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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

cription		68604	НОШО	Human	HOMO B	ALDSU622 Human DNA	Min min	Ratt	Rattus	Mus mu	Segue		sapiens m	uman STS	Oryctol	RVOKORGA GOLODKOOF	Homo sabi	AC120060 Rattus no	Rattus	Q :		AL049758 Human DNA	Hom	Mus	Mus	Homo	Ношо	Homo	HOHOU THE	ACCE/32 ACMO Sapi ACC84305 Homo sapi	Ratt	Rattus	ALB3355 HOMO SAD1 AL390211 Human DNA	Human	ношо в	Sequen	ALCOSTS HUMAN DNA	Human	ношо в			linear PAT 16-JUL-2002				Vertebrata; E	ni; Hominidae; Homo.	vectors containing them and
DB ID		AX46860										BD094076	HSRNAC	G286	AFIS	RVO	AC026	AC12(AC095	U7302	AC104	HSJ4	AC026	AC123	AC10	AC068	AC129	AC090	AC078	2 AC084305	AC137	AC096	PEWSH PER	BD09	AP003	AX035	HS41	AL162	AC04(ALIGNMENTS			Patent W00246220.	21901403	an)	a; Chordata; Craniata;	Primates;	llec,D. and Chien,K of the carp gene,
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TITLE Direct Submission JOURNAL Submitted (26-FBB-1999) Second Department of Internal Medicine.	Oy 661 GGGTGAGTTTGGGGA 	GTTTGGGGAGAAATAGACACACAAAGGTCAAACATAACTTCCTAATTAACACTT 720
SHOWA-MACHI, MAE	Qy 721 CCCTCCATTCACAATTCCCTTC	TCCCTTCTCCCATCTTCTCTCTGTCTTTACTSAKARAACCC 780
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Query Match Query Match Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 2074; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1021 TTTCTGACAAGCTCCC	GACAAGCTCCCACAGGTGATTCCTTTCCCCACAGCATTTGAGAACTTCAGCTCAA 1080
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181 GCCTGGAACAAAAGGCATACGAAATGGTAGAAAAGTGTCCATGACTACTTCTGACTTA 24	Qy 1261 CACCCGGCTGATAGCTGGTTT 	IGGTTTCATTTACTCTATTTCTTGACCACTCTGATCCATTTTGAA 1320
DD 181 GCCTGGAACAAAAGGCATACGAAATGGTAGAAAAGTGTCCATGACTTCTGACTTA 240	Oy 1321 GTAAAAATGCTCCAA	GIAAAAATGCTCCAATTATTATGCTGTTTTAGAACACGGTAAGCATGTCATGTGCTAATG 1380

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together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequence suith only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw.; SWISSROT; Tr.; TREMBL; Wp.; WORNPEP; Information the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10. Further information can be found at http://www.sanger.ac.uk/HGFC/LNIO

RPII-236Bls is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/Dacpac/home.htm
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/clone lib="RPCI-11.1"
a 32356 c 32839 g 46204
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Contact: humquery@sanger.ac.uk
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humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 23, 2002 this sequence version replaced gi:12191663.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
      GTAAAAATGCTCCAATTATTATGCTGTTTTAGAACACGGTAAGCATGTCATGTGCTAATG
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Bird, C.

REFERENCE AUTHORS TITLE JOURNAL

ORGANISM

KEYWORDS SOURCE

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3 TTC 1	AC074094 Homo sapiens chromosome SEQUENCE, 17 unordered AC074094 AC074094.3 GI:9958197		A (bases 1 to 160350) Materston, R.H. The sequence of Homo sapiens clone Unpublished 2 (bases I to 160350) Waterston, R.H. Direct Submission	ΑΓ	Center: Washington University Genome Sequencing Center Center: washington University Genome Sequencing Center Center code: WIGGE Web site:http://genome.wustl.edu/asc/index.shtml	Center project name: H_NH0236B18	Sequencing vector: plasmid; 0% Chemistry: Dye-primer ET; 100% of reads Chemistry: Dye-terminator Blg Dye, 0% of reads Assembly, ordered Phram version 0 9001s	Consensus quality: 149545 bases at least Q40 Consensus quality: 152532 bases at least Q30 Consensus quality: 153244 bases at least Q20 Treat size: 151000: squarescent	Insert size: 158750; sugarose-fig Quality coverage: 4.85 in Q20 bases; agarose-fp Quality coverage: 4.71 in Q20 bases; sum-of-contigs	* NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is anythrary. Gang hetween the contigs are represented as		2326: contig 2426: gap of 7519: contig	7520 7528; contig of 7654 bp in length * 15287 15386; gap of unknown length * 15387 23350; contig of 7664 bp in length	23150: gap or 33663: contig 33763: gap of 50133: contig	50233: 68088: 68188: 88133: 88233: 113397:	11 A 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
qa	RESULT 4 AC074094/C LOCUS DEFINITION ACCESSION VERSION	KEYWORDS SOURCE ORGANISM PEFEPENCE	KEFEKENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE	JOURNAL												
420 GAAATIAGTGATAGCTGTGTCCATCTCAAAGAAAAGCCCAGGAGATTTCCTTTATTTA	478 CCCCCTTTAAGATAGAACGGAACCAAATGATACAAAGGAGGTACTGGGAGGG 537	598 AACACCATCCACTGACTGAGGATTCAAGGGGAAGGGAATGGCAGCCACATTTGTTG 657	ATTGGGTGATTTGGGGAGAAATAGACACAAGAGGTCAAAAAAAA	CCCAGTITITCCTGAAACTATAAAAATACCCCCAGTATGTTTACATAATTTACACCTCAA	838 AGATTAGAAACCAGAAATAGAGACC-TTTTCAACCCTTCCGGAAGCAAGTGCATTATCC 896 	897 CTCCAGCCAGTGTCTCAAATCTTGATGCATCAGAATCATCTGGGTGCTTTKAAATTCAA 956 	957 GATGATTCCTACGAGTTACCATAAATCAACTCAGAATTCCCTGGAGTGGGG-CCAGGGAT 1015 	1016 CTGTATTTCTGACAGAGCTCCACAGGTGATTCCTTTCCCCACAGCATTTGAGAACTTCG 1075	1076 CTCAATGACCTAATCAGAGTCCTGCCATTGCTAATATCTGGTCTCATTTTTBTCATATT 1135 	1136 ATATATAGTATTTGTGGTAGAGATGGGATTTTGCCCATGTTGCCCAGGCTAGTATTGAACT 1195 	1196 CCTAAGCTAAGCAATCTTCCTGTCTCTGCCTCCCAAATGTTGGGATTACAGGTGTAAGC 1255 	1256 CACTGCACCCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTGACCACTCTGATCCATT 1315	1316 TIGAAGTAAAAATGCTCCAATTATTATGCTGTTTTAGAACACGGTAAGCATGTCATGTGC 1375	1376 TAATGGCCAGTGACATCATAAAAGAAAAGTGCATTACTGAATGCTTTCAATGTCTTA 1432 	1433 TAATGATGGTAAGGTGGCÄTGTCATGGGGCCTATTTAG-CCCAGACATCACTCCAAAGAA 1491 	

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114699 AATAGGAGCTATACAAAGAAGATTAGCATGGACTCTGTGCAAGAATGACACACAAATTTG 114640
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1398 113497: gap of unknown length 1498 14132: contig of 28235 bp in length 14132: gap of unknown length 14183: gap of unknown length 14387: contig of 1355 bp in length 143287: gap of unknown length 144942: contig of 1655 bp in length 1643 145042: gap of unknown length 147286: contig of 2244 bp in length 147386: contig of 2244 bp in length 147386: contig of 2466 bp in length 187357: contig of 3466 bp in length 18550: gap of unknown length 18557: contig of 2598 bp in length 187257: contig of 2993 bp in length 187357: gap of unknown length 187357
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153651. 157257
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157368. 160350
/note="assembly_name:Contig9"
0 a 32724 c 33135 g 45498 t 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .2326
/note="assembly_name:Contig10"
2427. .7519
/note="assembly_name:Contig11"
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141833. .143187
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143288. .144942
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145043. .147286
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/db xref="taxon:9606"
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/clone="RP11-236B18"
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/evidence=not_experimental
join(391. .472_3273. .3328,3962. .4018,4428. .4502,7467. .7538,
14216. .14305,23179. .23295,23858. .23887,24284. .24321,
24717. .24796,28974. .29083)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VÄVFPKTEKLFHIACTHLDVDLVCITVTEKLPFYFKRPPINVAIDRGLAFELVYSPAI
KDSTWRRYTISSALNLMQICKGKNVIISSAAERPLEIRGPYDVANLGLLFGLSESDAK
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24284. .24321,24717. .24796,28974. .29381)
gene="bh320815.1"
                                 IMPORTANT: This sequence is not the entire insert of clone RPII-320FIS It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RPII-236BI8 is at 5012 in this sequence. The true right end of clone RPII-103A2 is at 100 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(120. 472,3273. 3328,3962. 4018,4428. 4502,7467. 14216. 14302,23179. 22295,23858. 23887,24284. 24321, 24717. 24796,28974. 29381)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="ba320F15.1.1 (ribonuclease P (30kD) (RPP30))"
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match: ESTs: Em:BE572689 Em:BE374859 Em:BE137893
Em:A9220575 Em:BG106620 Em:BF681617 Em:BF248001
Em:BF031745 Em:AA854455 Em:A1359795"
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/note="L2 repeat: matches 2557. .2696 of consensus"
2939. .3167
/note="MIR repeat: matches 13. .262 of consensus"
complement (4176. .4649)
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/note="L2 repeat: matches 2459 .2502 of consensus"
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note="match: ESTs: Em:AW939965"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-11.2"
complement(1. .98)
/note="match: GSS: Em:AQ670367"
complement(1. .97)
/note="match: GSS: Em:AQ544636"
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note="match: GSS: Em:AQ626500"
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                                                                                                                                                                                                                                                                                              l. .50111
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic_DN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /chromosome="10"
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                                                                                                                                                                                                                                                         Location/Qualifiers
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/note="match: STS:
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/gene="bA320F15.1"
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/gene="bA320F15.1"
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During sequence assembly data is compared from overlapping clones.

Mere differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following aboreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr:, TREMBL; WP: NORMBEP; Information on the WORMBEP that their source databases: Em; EMBL; Sw; Although their source dat
                                                                                                                                                                                                                                                         113800 CCTAAGCTAAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAGC 113741
                                                                                                         1433 TAATGATGGTAAGGTGGCATGTCATGGGGCCTATTTAG-CCCAGACATCACTCCAAAGAA 1491
                                                                                                                                                                                                                                                                                                                                                              1376 TA---ATGGCCAGTGACATCATAAAAGAAAAGTGCATTACTGAATGCTTTCAATGTCTTA 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1492 TTCCAAACAGATATAGACAAGTGCCTTTAGGGCCCAGATCCCTTCCCCTCAGGCTGTTTA 1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALS90622 50111 bp DNA linear PRI 19-SEP-2001 Human DNA sequence from clone RPI1-320F15 on chromosome 10. Contains the gene for ribonuclease P 30kD subunit, the gene for an unclear protein similar to CARP, ESTS, STSS and GSSS, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uf.kfGP/Chr10 RP11-320F15 is from the library RPCI-11.2 constructed by the group of Piter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 50111)

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                                                                       CACTGCACCCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTGACCACTCTGATCCATT
                                                                                                                                                                                                               1316 TTGAAGTAAAAATGCTCCAATTATTATGCTGTTTTAGAACACGGTAAGCATGTCATGTGC
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complement (25417. .25863)
/note="match: GSS: Em:AQ712354"
26204. .26603
/note="LiMA2 repeat: matches 5888. .6302 of consens: 28442. .28516
/note="LiZ repeat: matches 2636. .2710 of consensus" 29149. .29154
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Pred. No. 9.2e-141;
0; Mismatches 2;
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/gene="bA320F15.1"
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Best Local Similarity 99.6%;
Matches 677; Conservative
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join(23179. 23295,23858. 23887,24284. .24321,24717. .24796,

28974. .29072,30647. .30748,31596. .31680,33706. .34469)

/gene="bA320F15.13" (putative isoform 3)"

/product="bA320F15.13" (putative isoform 3)"

/note="match: EST8: Em:BE567341 Em:AI292002 Em:BF684192

Em:BF435407 Em:AI740881 Em:AA651912 Em:BF438915"

/evidence=not_experimental

/gene="bA320F15.1"
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/note="MIR repeat: matches 76. .212 of consensus"
10798. .11076
/note="MIR repeat: matches 1. .291 of consensus"
11086. .11219
/note="FLAM C repeat: matches 1. .129 of consensus"
11319. .11491
/note="MIR repeat: matches 3. .189 of consensus"
11928. .11984 repeat: matches 1743. .1801 of consensus"
11955. .13817
/note="Lz repeat: matches 2684. .2749 of consensus"
13755. .13817
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/note="match: GSS: Em:B53566"
25321. .25458
/note="FLAM_C repeat: matches 1. .133 of consensus"
                                                  .2732 of consensus"
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complement(join(24284. .24321,24724. .24796,28974.
/note="match: STS: Em:G24365"
                                                                                                                                       .1971 of consensus"
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                                                                                                                                                                                                                                                                       .312 of consensus"
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/note="2 copies 81 mer 81% conserved"
8445. .8541
8542. .8583
/note="HY1 repeat: matches 16. .112 of consensus"
/note="HY1 repeat: matches 1. .42 of consensus"
                                                                                           .2478 of
         4928. .5102

'note="L2 repeat: matches 2601.

'note="L2 repeat"
                                                       ...ve="L2 repeat: matches 2299.
5257. .5439
'note="L2 rene"*
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/note="AluSx repeat: matches 7.
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884. 7196
note="AluJb repeat: matches 1.
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24561. .24956
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gene="bA320F15.1"
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/note="L2 re
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                         Sequences upstream of the carp gene, vectors containing them and
uses thereof
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Aventis Pharma S.A. (FR); The Regents of The Unive
California at San Diego (US); Benoit, Patrick (FR)
Location/Qualifiers
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PRESENT. 7

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* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* 1 61126: contig of 61126 bp in length

* 61127 142205: contig of 81676 bp in length.

Location/Qualifiers
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                                                                                                              /clone_lib="RPCI-24 Male Mouse BAC"
30899 c 29987 g 40473 t 167 others
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                                                                                            Web site: http://www-seg.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="genomic DNA"
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/clone="RP24-211P24"
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Best Local Similarity 76.4%;
Matches 597; Conservative
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AL SUBMILLEAUCH SOLOR) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:23101653.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contigs scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
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NOTE: This is a "working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (09-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Center project Information
Center clone name: GNAG
Center clone name: CH230-140118
Assembly program: Phrap; version 0.990329
Consensus quality: 215126 bases at least Q40
Consensus quality: 218436 bases at least Q30
Consensus quality: 21866 bases at least Q20
Estimated insert size: 214300; sum-of-contigs estimation
Quality coverage: 10x in Q20 bases; sum-of-contigs estimation
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,A., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wieczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
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Contact: hgsc-help@bcm.tmc.edu
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Rat Genome Sequencing Consortium
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141673 ----CTTCCCCCCGGGCTGTTTATTCCCAGGAATAGGATGTCCCAAAGCAACACTTCCA 141727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141728 GGCCAACTGGAGTGCTGATAAGCCCAGTTATCAGAAAGATATTGCCGTGAGTGTGATGCA 141787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1702 GCAGTGATGTGGTGCAATGTCAACAGACGGTGTCCCTGACTCTTGACAATAGGATGA 1761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1289 TCTATTTCTTGACCACTCTGATCCATTTTGAAGTAAAATGCTCCAATTATTATGCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141439 TGTGTCTCTGGACCACTCTGACCCATTTTGAGGTCAATAT--TCCGATTAGCCTTCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1349 TTAGAACACGGTAAGCATGTCATGTGCTAATGGCCAGTGACATCATAAAAGAAAAGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141497 TTAGAGCAC----ATGCCATGCACTAATTATGGCCAGTGACACCATAAAGTAAAAGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141553 TTACTGAATGCTTTCAATTTCTCATAATGATGGTAAGGTGGCGTGTCATGGGGGCCATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1644 TAGGGCATCTACATTTTCTTGATAGGTAGTCATATGAAAGCTGACAAAAGAA-AAAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCCC-AGACATCACTCCAAAGAATTCCAAACAGATATAGACAAGTGCCTTTAGGGCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 229640;
               224771: contig of 1611 bp in length 224871: gap of unknown length 225886: contig of 1015 bp in length 225986: gap of unknown length 1228380: gap of unknown length 228380: gap of unknown length 229640: contig of 1360 bp in length.
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length
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4765._.7050
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/organism="Rattus norvegicus"
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Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Alsbrooks, S., Amin, A., Anguiano, D., Angalebechii, V., Aoyagi, A., Aydogii, M., Baca, E., Badeh, H., Badatebechii, V., Aoyagi, A., Aydogii, M., Barnstead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bandhui, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cradenas, V., Carter, M., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chen, Z., Chen, S., Chen, R., Chen, Y., Chen, Z., Chen, Z., Chen, S., Davano, C., Davano, S., Deramo, C., Dinh, H., Divya, K., Davala, M. L., Davis, C., Derson, S., Deramo, C., Bunch, R., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Dinh, H., Divya, K., Egan, A., Escotto, M., Elago, V., Pannadez, S., Fillay, M., Flago, V., Pannadez, S., Fillay, M., Flago, V., Pannadez, S., Fillay, M., Flago, V., Parnandez, S., Fillay, M., Haderson, N., Herrandez, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevar, W., Harnder, M., Handlin, S., Halak, P., Handerson, N., Henderson, N., Hernandez, M., Hollins, S., Huladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howellis, S., Huladun, S.L., Hodgson, A., Hogues, M., Margathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Lewan, J., Lewis, L., Liu, W., Liu, Y., London, P., Longacre, S., Morgan, M., Mahindarthe, M., Mahindar, B., Manda, M., Malloy, K., Margh, S., Margh, S., Markevis, C., Neta, M., Markin, M., Martin, Ren, M., Morris, S., Markevis, C., Neta, M., Perez, A., Milosavijevic, A., Miner, G., Olarmpunsagoon, A., Pallak, S., Pall, H., Perez, A., Perez, L., Petander, S., Pally, M., Perez, A., Perez, M., Reigh, R., Petande, S., Reigh, R., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Reigh, R., Reigh, R., Reigh, R., Reigh, R., 
                                                                                               141847 GCAGCGATGTGGTGCAATATGAACAGGCAGCTGTCCCTGGCTTCCCGATAAGTAGGATGA 141906
                                                                                                                                                                                                                     1762 CTTGCATTGCTGAGCGATGTGATCACCACCAAAGGAATGGCCCTCTCACATTTCTTCCTG 1821
                                                                                                                                                                                                                                                                                                                                                                                                                                     1942 TTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCGGTGT 2001
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*** SEQUENCING IN PROGRESS ***,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002 GGAGGGGCCCAGCAGGGCCAACTCCAGGGATTCCTTC-CACGACAAAACATACA 2057
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Rattus norvegicus clone CH230-26A2,
2 unordered pieces.
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HTG; HTGS_PHASE1; HTGS_DRAFT; F
Rattus norvegicus (Norway rat)
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Submitted (14-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 14, 2002 this sequence version replaced gi:22855482.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each conrig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, T., Thomas, M., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaeana, D., Waldron, L., Walker, B., Wang, J., Walght, D., Wilson, R., Wleczyk, R., Wei, X., White, F., Wilson, R., Wleczyk, R., Weden, H., Worley, K., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Wainstock, G. and Gibbs, R.A.
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* CONSISTS Of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Worley, K.C.
Direct Submission
Submitted (11-071-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
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Direct Submission
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1. (bases 1 to 723)

S. Maeda, T., Sepulveda, J., Chen, H.H. and Stewart, A.F.R. alphal-Adrenergic activation of the cardiac ankyrin repeat protein gene in cardiac myocytes

Gene 297 (1-2), 1-9 (2002)

E. 2 (bases 1 to 723)

S. Maeda, T., Sepulveda, J. and Stewart, A.F.R.

Direct Submission

Location (209-JAN-2002) Cardiovascular Institute, University of Pittsburgh, 200 Lothrop Street, Pittsburgh, PA 15213, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TTACTGAATGCTTTCAATTTCTCCTAATGCTGGTACGATGGCATGTCACAGGGCCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AGCTGCAGACATCACTCCAGAGAATTCCAAACAGATAGAGACAAGTGGCACCCAGACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1528 GATCCCTTCCCCTCAGGCTGTTTACCCAGGGAATAGGATGTCCTGGGACAAGTTTCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 TCTCCTTCCCCTCGGCTGATTATCCCCAGAATAGATGCTCCCAAAGCAACTTCCCAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="cardiac ankyrin repeat protein"
721. >723
/gene="Carp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon start=1
/product="cardiac ankyrin repeat protein"
/protein id="AAL85342.1"
/db_xref="G1:19110907"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.4%; Score 340.8; DB 10; Length ilarity 74.0%; Pred. No. 5.2e-67; Conservative 0; Mismatches 172; Indels
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    .723
    /organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
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1. .720
/gene="Carp"
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/gene="Carp'
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Matches 527;
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                                                                                                                                                                                                                                                                                                                                                                                           TTACTGAATGCTTTCAATGTCTTATAATGATGGTAAGGTGGCATGTCATGGGGGCCTATTT 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCCC-AGACATCACTCCAAAGAATTCCAAACAGATATAGACAAGTGCCTTTAGGGCCCCA 1527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1644 TAGGGCATCTACATTTTCTTGATAGGTAGTCATATGAAAGCTGACAAAGGA--AAAAAGG 1701
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                                                                                                                                                                                                                                                    1289 TCTATTTCTTGACCACTCTGATCCATTTTGAAGTAAAAATGCTCCAATTATTATGCTGTT
                                                                                                                                                                                                                                                                                                         1349 TTAGAACACGGTAAGCATGTCATGTGCTAATGGCCAGTGACATCATAAAAGAAAAGTGCA
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                                                                                                                                                                                      Gaps
                                                                                                                                                                                      26;
                                                                                                                                         Query Match 17.6%; Score 365; DB 2; Length 238344; Best Local Similarity 77.3%; Pred. No. 1.4e-72; Matches 601; Conservative 0; Mismatches 150; Indels 26;
                                                                                 6855 others
                                                                             71429 t
db_xref="taxon:10116"
                                                       /note="wgs_contig"
47381 c 49225 g
            /clone="CH230-26A2"
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RESULT 10 AF478692

ACCESSION VERSION KEYWORDS SOURCE

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (Dassa 1 to 1901)

Sakurada,K., Yoshisue,H., Obayashi,M., Ota,T., Kawabata,A., Sakurada,K., Kuga,T., Sekine,S., Nakamura,Y. and Sugan,S.

Shear stress-responsive DNAs

L. Patent: WO 012547-A 37 12-APR-2001;
KYOWA HAKKO KOGYO CO LTD,HIROSHI NOJIMA,HAJIME YOSHISUE, MASAYA
OBAYASHI, TOSHIO OTA,AYAKO KAWABATA,KAZUHIRO SAKURADA,TETSURO KUGA,SUSMU SEKINE, YUSUKE NAKAMURA,SUMIO SUGANO
OS HOmo sapiens (human)
PD 12-APR-2001
PP 02-OCT-2000 WO 2000JP006840
PR 01-OCT-1999 JP 99P 280976
PR HIROSHI NOJIMA,HAJIME YOSHISUE,MASAYA OBAYASHI,TOSHIO OTA, PI
                                                                                                                                                                                                                                                                        HIROSHI NOJIMA, HAJIME YOSHISUE, MASAYA OBAYASHI, TOSHIO OTA, PI AYAKO KAWABATA, TOSHISUE, WASAYA OBAYASHI, TOSHIO OTA, PI AYAKO KAWABATA, TETSURO KUGA, SUSUMU SEKINE, YUSUKE NAKAMURA, PI SUMIO SUGANO PC C12NIS/12, COTK14/435, COTK16/18, C12P21/02, C12Q1/68. P. CC AGIX39/395, PC AGIX39/395, PC AGIX39/395, PC AGIX39/395, PC CC TI CT AGIX39/395, PC AG
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Butheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.0%; Score 228; DB 6; Length 19
Best Local Similarity 97.6%; Pred. No. 2.3e-41;
Matches 242; Conservative 0; Mismatches 5; Indels
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
378 c 460 g 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1828 ATATTCAGCAGGGTTAGCTTGT-
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Homo sapiens (human)
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                                                                                                                                   TTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGG
CATAITCAGCAGGGITAGCTIGICCICCCCTCCCTCTTCAGCTICCCAGACACAGAGTCI
                                                 CATACGCCGCGG-----CCAGCTTGTCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCT
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Novel target genes for diseases of the heart
Patent: WO 0192567-A 19 06-DEC-2001;
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a 378 c 460 g 471
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Sequence 19 from Patent WO0192567.
AX322775
AX322775.1 GI:18093755
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Location/Qualifiers
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Matches 242; Conservative
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AX322775
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BD094076
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-- Washington University/Merck EST sequence.
Location/Qualifiers
                                          Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
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seconds
                                                                                                                                                                                                                                                                                                                                                    Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                          Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1901;
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62 degrees C for 23 si
72 degrees C for 30 si
30
Perkin Elmer 9600
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each 200 uM
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/organism="Homo sapiens"
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Primer B: CCAGATGGATGATCATGAAGG
STS size: 222
PCR Profile:
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378 c 460 g 4
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Fax: 4157259689
Email: myers@shgc.stanford.edu
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                                        Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
1 (bases 1 to 1901)
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50
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8.3
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Total Vol:
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Polymerization:
PCR Cycles:
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          Homo sapiens (human)
                                                                                          Myers, R.M.
Unpublished (1996)
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Matches 242; Conservative
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LSTALHVAVRTGHYECAEHLIACEADLNAKDREGDTPLHDAVRLNRYKMIRLLIMYGA
DLNIKNCAGKTPMDLVLHWQNGTKAIFDSLRENSYKTSRIATF"
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                                                                                                  Direct Submission
Submitted (05-JAN-1995) W. Chu, Hoffmann-La Roche, 340 Kingsland
Street, Dept. of Inflammation/Autoimmune Disease, Hoffmann-La
Roche, Nutley, NJ 07110, USA
Location/Qualifiers
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11.0%; Score 228; DB 9; Length 1901;
Best Local Similarity 97.6%; Pred. No. 2.3e-41;
Matches 242; Conservative 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="cytokine-inducible expression"
nuclear protein from human endothelial cells J. Biol. Chem. 270 (17), 10236-10245 (1995) 95247734
                                                                                                                                                                                                                                                                                                                                                                                    /note="nuclear localization signal"
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CEGHLAIVEKLMEAGAQIERPUMLESTAIHWACRGNLEVLKLLLNKGAKISARDKL
LSTALHVAVRTGHYECAEHLIACEADLNAKDREGDTPLHDAVRLNRYKMIRLIIMYGA
DLTIKNSAGKTPHULNWQWYTKAIFDSLKENSYKTSRIATF"

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                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.

1 (bases 1 to 1940)
Aihara, Y., Kurabayashi, M., Arai, M., Kedes, L. and Nagai, R.
Molecular cloning of rabbit CARP cDNA and its regulated expression
in adriamycin-cardiomyopathy
Biochim. Biophys. Acta 1447 (2-3), 318-324 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (Dases 1 to 1940)
Aihara,Y.
Direct Submission
Submitted (26-PEB-1999) Second Department of Internal Medicine,
Gunma University School of Medicine, 3-39-15 Showa-machi, Maebashi
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                                                                                                                                                           AF131883 1940 bp mRNA linear Oryctolagus cuniculus CARP mRNA, complete cds. AF131883
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Location/Qualifiers
1 1.940
/organism="Oryctolagus cuniculus"
/mol_type="mRNA"
/db_xref="taxon:9986"
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LOCUS
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(REGC ) UNIV CALIFORNIA.
(BENO/) BENOIT P.
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Human polynucleoti
Human shear stress
Human CAA58676 pro
Human DNA sequence
Differentially exp
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Mouse CARP protein
                                                                                                                                          November 17, 2003, 23:28:30; Search time 543.77 Seconds (without alignments) 10295.963 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                       1 ctgcagcaagttacttaatg......acaagactccttcagccaac 2074
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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2552756 segs, 1349719017 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 nucleic search, using sw model
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Perfect score:
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322.6
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228
144.4
144.4
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Human immune/haema
Genomic sequence #
Human immune/haema
Human immune/haema
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Human nervous syst
Human nervous syst
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Human immune/haema
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cDNA encoding nove
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                                                                                                                                                                                                                                                               Human musculoskele
                                                                                                                                                                                                                                                                                                                                                                                                                                           Cardiac ankyrin repeat protein; CARP; cardiant; immunosuppressive; antiinflammatory; gene therapy; antisense gene therapy; human; ds.
Human
                                                                                                                                                                                                                      Human
                                                                                                                                                                                                                                                                                                                                                                                                                           Human CARP protein coding sequence upstream DNA fragment.
                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                  ABA16110
ABK87050
AAK60063
AAK85377
AAK85378
                                                                                                                                                                                                                     AAK65595
AAK65596
AAK65597
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AAC81712
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26390
56737
5248
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5249
118384
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52845
23329
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4678
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4. 4. 4.
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Chien K;

New promoter sequence derived from a portion upstream of the coding sequence of a gene for Cardiac Ankyrin Repeat Protein, for controlling the level and specificity of expression of a transgene in cardiac muscle cells

Claim 5; Fig 2; 48pp; English

The invention relates to a polynucleotide (I) comprising a fragment of a sequence upstream of the coding part of the gene for the Cardiac Ankyrin (Repeat Protein (CARP). (I) is capable of inducing a specific expression in vivo of a gene operably linked to (I), in cardiac cells. (I) or a vector (IIb) comprising (I) is useful for the manufacture of a medicament intended for the treatment of cardiac insufficiency, cardiac hypertrophy and hypoxia, and for preventing rejection during cardiac transplant. An expression cassette under the control of (I) is useful for encoding a protein or RNA which is capable of activating the growth of cardiac cells, reducing or suppressing an immune response, inducing angiogenesis, correcting muscle contractility, cardiac hypertrophy, cardiac cardiac correcting muscle contractility, aseful for expressing a gene of therapeutic interest in vivo, by isolating (IIb) and introducing (IIb) in the cardiac tissue, under conditions so that the gene of interest is caparentian of cardiac pathologies. (I) is also useful for generating transgenic animals which constitute models for studying certain cardiac prevention of cardiac pathologies. (I) is also useful for screening molecules for their activity on the regulatory sequences of the gene centeding the CARP protein. The present sequence represents the DNA fragment upstream of the coding sequence of a human CARP protein.

Sequence 2074 BP; 612 A; 469 C; 416 G; 572 T; 5 other;

GTCTTGCTCCAACTTCGAGGGCATGGACAGCTCTGGGATTTCATATCCAAGACCCTTAAA 120 180 240 240 300 360 480 CCTTTAAGATACAATATTAGGAGACCGGAACATATGATACAGGAGGTACTGGGAGGTCC 540 GTCTTGCTCCAACTTCGAGGGCATGGACAGCTCTGGGATTTCATATCCAAGACCCTTAAA 120 241 GATGAAGAGACCAATGAAAATAGTAATGACTCTGTTTGCTTCAGCAGGACATATACTAAA 300 GAAACATTCCATATATAAAATAAATAAATAATAATAAGAGAAAAGGAAAAATTAAAAAG 420 541 CTCTTTGTCAATGTTTTGTCTTGGGGTGGGGAGTCGATGTCTTCTCAAAGTTTCAGAAAC 600 09 GCCTGGAACAAAAAGGCATACGAAATGGTAGAAAAAAGTGTCCATGACTACTTCTGACTTA 1 criccaccaagriacriaargriririrgccricagcarccricrigiaaaargagagcarra 181 GCCTGGAACAAAAAGGCATACGAAATGGTAGAAAAAGTGTCCATGACTACTTCTGACTTA GATGAAGAGACCAATGAAAATAGTAATGACTCTGTTTGCTTCAGCAGGACATATACTAAA ATAGGAGCTATACAAAGAAGATTAGCATGGACTCTGTGCAAGAATGACACACAATTTGT ccrrraagaragararraagaccegaacararargaracaggaggregracregegaggrecc CTGCAGCAAGTTACTTAATGTTTTTTGCCTCAGCATCCTCTCTGTAAAATGAGAGCATTA Gaps DB 24; Length 2074; . 0 0; Indels Query Match
99.9%; Score 2071.6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2074; Conservative 0; Mismatches 361 61 181 241 301 301 421 481 481 61 121 361 421

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δλ	601	ACCATCCACTGACTGAGCATTCAAGGGGCAAGGAGAATGGCAGCCACATTTGTTGATT 660
Dp	601	Accarccacrdacrdacarrcaagggcaagaaggaarggcagccacarrrgrrgarr 660
δ	661	GGGTGAGTTTGGGGAGAAATAGACACACAAAGGTCAAACATAACTTCCTAATTAACACTT 720
QQ	661	GGGTGAGTTTGGGGAGAAATAGACACACAAAGGTCAAACATAACTTCCTAATTAACACTT 720
8	721	CCCTCCATTGACAATTCCCTTCTCCCCATTCTTCTCTCTGTCTTTTACTSAKARAAACCC 780
qq	721	CCCTCCATTCACAATTCCCTTCTCCTTCTTCTTCTTTTTT
δλ	781	AGTTTTTCCTGAAACTATAAAAATACCCCCAGTATGTTTACATAATTTACACCTCAAAGA 840
qq	781	AGTTTTTCCTGAAACTATAAAATACCCCCAGTATGTTTACATAATTTACACCTCAAAGA 840
δλ	841	TTAGAAACCAGAAATAGAGACCTTTTCAACCCTTCCGGAAGCAAAGTGCATTATCCCTCC 900
qq	841	TTAGAAACCAGAAATAGAGACCTTTTCAACCCTTCCGGAAGCAAAGTGCATTATCCCTCC 900
λO	901	AGCCACGTGTCTCAAATCTTGATGCATCAGAATCATCTGGGTGCTTTKAAATTCAAGATG 960
qa	901	AGCCACGTGTCTCAAATCTTGATGCATCAGAATCATCTGGGTGCTTTKAAATTCAAGATG 960
δ	961	ATTCCTACGAGTTACCATAAATCAACTCAGAATTCCCTGGAGTGGGGCCAGGGATCTGTA 1020
qa	961	ATTCCTACGAGTTACCATAAATCAACTCAGAATTCCCTGGAGTGGGGCCAGGGATCTGTA 1020
ò	1021	TITCIGACAAGCICCCACAGGIGATICCTITCCCCACAGCATITGAGAACTICAGCTCAA 1080
qq	1021	TTTCTGACAAGCTCCCACAGTCGTTCCCTTTCCCCACACTTTGAGAACTTCAGCTCAA 1080
δλ	1081	TGACCTAATCAGAGTCCTGCCATTGCTAATATCTGGTCTCATTTTBTCATATATATAT
Dp	1081	TGACCTAATCAGAGTCCTGCCATTGCTAATATCTGGTCTCATTTTTBTCATATATATA 1140
ò	1141	TAGTATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAACTCCTAA 1200
qq	1141	TAGTATTTGTGGTAGGATTTTGCCATGTTGCCCAGGCTAGTATTGAACTCCTAA 1200
λŏ	1201	GCTAAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAAGCCACTG 1260
Db	1201	GCTAAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAGCCACTG 1260
δλ	1261	CACCCGGCTGATAGCTGGTTTACTTTACTTTTTTTTGACCCCTCTGATCCATTTTGAA 1320
ΩÞ	1261	caccederigaraderedritrarritaererarreredeceaereredrecarritraa 1320
λo	1321	GTAAAAATGCTCCAATTATTATGCTGTTTTAGAACACGGTAAGCATGTCATGTGCTAATG 1380
QQ	1321	GTAAAAATGCTCCAATTATTATGCTGTTTTAGAACACGGTAAGCATGTCATGTGCTAATG 1380
ò	1381	GCCAGTGACATCATAAAAAGAAAAGTGCATTACTGAATGCTTTCAATGTCTTATAATGATG 1440
ДD	1381	GCCAGTGACATCATAAAAGAAAAGTGCATTACTGAATGCTTTCAATGTCTTATAATGATG 1440
λŏ	1441	GTAAGGTGGCAIGTCAIGGGGCCTAITTAGCCCAGACAICACTCCAAAGAAITCCAAACA 1500
qq	1441	draagsiggcargicarggggccraftragcccagacarcacrccaaagaarrccaaaca 1500
ολ	1501	GATATAGACAAGTGCCTTTAGGGCCCAGATCCCTTCCCCTCAGGCTGTTTACCCAGGGAA 1560
QQ	1501	GATATAGACAAGTGCCTTTAGGGCCCCAGATCCCTTCCCCTCAGGCTGTTTACCCCAGGGAA 1560
δŷ	1561	TAGGATGTCCTGGGACAAGTTTCCCCTAAGTGAAGTGTTGATAAGTCTGCTTATCAGAAA 1620
Dp	1561	TAGGATGTCCTGGGACAAGTTTCCCCTAAGTGAAGTGTTGATAAGTCTGCTTATCAGAAA 1620
٥٨	1621	.621 GATATTACTGGGGGTGTGATATGTAGGCGTTCTACATTTTCTTGATAGGTAGTAGTATGA 1680

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a polynucleotide (I) comprising a fragment of a sequence upstream of the coding part of the gene for the Cardiac Ankyrin Repeat Protein (CARP). (I) is capable of inducing a specific expression in vivo of a gene operably linked to (I), in cardiac cells. (I) or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New promoter sequence derived from a portion upstream of the coding sequence of a gene for Cardiac Ankyrin Repeat Protein, for controlling the level and specificity of expression of a transgene in cardiac
                      1801 GCCCTCTCACATTTCTTCCTGATTCACATATTCAGCAGGGTTAGCTTGTCCTCCCCTCCC
                                                                            GCCCTCTCACATTTCTTCCTGATTCACATATTCAGCAGGGTTAGCTTGTCCTCCCCTCCC
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                                                                                                                                                                        1921 TAATGGGGGGGGGGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCA
              Cardiac ankyrin repeat protein; CARP; cardiant; immunosuppressive; antiinflammatory; gene therapy; antisense gene therapy; mouse; ds.
                                                                                                                                                                                                                                                                                                           Mouse CARP protein coding sequence upstream DNA fragment.
                                                                                                                                                                                                      Chien K;
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correcting or suppression (I) is useful for the manufacture of a medicament intended for the treatment of cardiac insufficiency, cardiac hypertrophy and hypoxia, and for preventing rejection during cardiac transplant. An expression cassette under the control of (I) is useful for encoding a protein or RNA which is capable of activating the growth of cardiac cells, reducing or suppressing an immune response, inducing angiogenesis, correcting muscle contractility, cardiac hypertrophy, cardiac chrappentic interest in vivo, by isolating (IIb) and introducing (IIb) in the cardiac tissue, under conditions so that the gene of interest is cypressed. (I), the vectors and the compositions are useful in clinical, expressed. (I), the vectors and the compositions are useful in clinical, cypremation of cardiac pathologies. (I) is also useful for generating transgenic animals which constitute models for studying certain cardiac pathologies. (I) is also useful for screening concluding the CARP protein. The present sequence represents the Dance concoding the CARP protein. The present sequence represents the DARP protein.
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                                                                           TATAGACAAGTGCCTTTAGGGCCCAGATCCCTTCCCCTCAGGCTGTTTACCCCAGGGAATA
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     GTGTGGAGGGCCCCAGCAGGGCCAACTCCAGGGATTCCTTC-CACGACAGAAAACATAC 2056
                                              2250 GTGTGGAGGGGCTCCACAGGGCCAGTTCCAGGGGTTCATCCACAAGAGAGAAAAACATAG 2309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ankyrin repeat protein; CARP promoter; murine; adenovirus vector; specific; heart disease; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a human type-5 recombinant adenovirus vector for achieving cardiac-restricted transcription of a gene of interest. The vector comprises inverted terminal repeat (ITR) sequences from human adeno-associated virus (AAV) type 2 (AAA10404-A10405) and a cardiac tissue-specific promoter. In particular, the promoter is that of the cardiomyocyte-restricted cardiac ankyrin repeat protein (CARP) gene. The adenovirus vector is used for targetted gene therapy for heart disease and for evaluating gene function. Cardiac restricted transcription of a transgene in both neonatal and mature cardiac tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1325 AAATGCTCCAATTATTATGCTGTTTTAGAACACGGTAAGCATGTCAT--GTGCTAATGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    can be achieved to treat inherited and acquired heart diseases. The vector is suitable for tissue-specific use in vivo and in vitro and provides cardiac restricted transcription. The present sequence represents the murine cardiac antyrin repeat protein (CARP) promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human type-5 recombinant adenovirus vector used for targeted gene therapy for heart disease and evaluating gene function contains a tissue-restricted promoter and inverted terminal repeat sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.6%; Score 322.6; DB 21; Length 2247; 76.3%; Pred. No. 2.5e-65; tive 0; Mismatches 154; Indels 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 2247 BP; 609 A; 549 C; 485 G; 589 T; 15 other;
                                                                                                                                                                                                                                                                                                                                                                                                                              Murine cardiac ankyrin repeat protein (CARP) promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Page 29-30; 33pp; English.
                                                                                                                                                                                                                                                                               DNA; 2247 BP
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Matches
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Human, congestive heart failure, dilative cardiomyopathy, sudden death, hypertrophic cardiomyopathy, ischaemic cardiomyopathy, rhythm disorder, heart muscle disease; conduction disorder; coronary heart disease; systemic arterial hypertension; pulmonary hypertension; endocarditis; pulmonary heart disease; valvular heart disease; pericardial disease; congenital heart disease; gene therapy; syncope; transgenic animal; expressed sequence tag; EST; clone X83703; CAA58676 protein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCCCAGCAGGCCAACTCCAGGGATTCCTTCCACGAAAAAACATACAAGACTCCTT
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                                                                                                              Sakurada K;
                                                                                                                                                                                                                                             DNA sequences, proteins encoded by them and antibodies against them useful in diagnosis and treatment of vascular disease caused by arteriosclerosis -
                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of a number of human shear stress response proteins. These are useful in diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1901;
                                                                                                              Kawabata A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1901 BP; 592 A; 378 C; 460 G; 471 T; 0 other;
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Pred, No. 2.8e-43;
0; Mismatches 5;
                                                                                                            M, Ota T,
Sugano S;
                                                                                                                                                                                                                                                                                                                                     Claim 20; Page 422-425; 678pp; Japanese.
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250..1209
                                                                                                            H, Obayashi
Nakamura Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                           (KYOW ) KYOWA HAKKO KOGYO KK
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Best Local Similarity 97.6%;
Matches 242; Conservative
  99JP-0280976.
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                                                                                                            H, Yoshisue, Sekine S,
                                                                                                                                                                          WPI; 2001-266308/27
P-PSDB; AAB90787.
                                                                NOJI/) NOJIMA H.
01-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypertension
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                                                                                                            Nojima H,
Kuga T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
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                                                                                                                                                                                                               The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA019910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                   Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.1%; Score 229.6; DB 22; Length 1988; 98.0%; Pred. No. 1.2e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                      Claim 1; SEQ ID NO 13568; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human shear stress-response coding sequence SEQ ID NO: 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 225.0,
Pred. No. 1.2e-43;
Pred. ----hes 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stress-response protein; vascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1988 BP; 632 A; 384 C; 472 G; 500 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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arteriosclerosis; ds
                    WPI; 2001-514838/56
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Matches 145; Conservative
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AAS94903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a subject at risk for a heart disease e.g. congestive heart failure, dilative cardiomyopathy, heart muscle disease, by quantifying the polypeptide expressed by genes abnormally expressed in heart tissue
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Pred. No. 2.8e-43;
0; Mismatches 5; Indels 1.
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                                                                                                                                                                                                                          1391..1401
//tags b
//totes 'AU-rich mRNA decay element"
1415..1423
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/product= "Human CAA58676 protein"
198..431
                                                                                                              *tag= b
'note= "S1MC01-1 cDNA fragment"
    / rag= b //note= "66268 cDNA fragment" | 1604..1753 //note= b //note= h
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Best Local Similarity 97.6%;
Matches 242; Conservative
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P-PSDB; AAE16633.
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                                                                                         1929 GCGGGGGGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATA
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WO200116311-A1.
                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                            31-MAY-2001
                                                                                                                                                                                                                                                                       08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nvention
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                                                                                                    AAF97854;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGGGAGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATA 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a combination of cDNAs (designated BC-CDNAs), which are differentially expressed in breast cancer. The combination includes 152 cDNA sequences, or their complements. The protein encoded by any of these BC-CDNAs is useful for screening several molecules or compounds to identify at least one ligand that specifically binds the protein, producing or preparing polyclonal or monoclonal antibodies, or bind the protein differentially expressed in breast cancer is useful for detecting the expression of a protein in a sample. The BC-CDNAs are also useful for diagnosing, monitoring the treatment of, or staging, breast cancer. This sequence represents a differentially expressed breast cancer associated CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGGAGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at seqdata.uspto.gov/sequence.html?DocID=20020156263.
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Pred. No. 8.9e-24;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer useful for diagnosing or staging, breast cancer, or for monitoring the treatment of breast cancer in an individual -
                                                                                                                                                                                                                                                                                                                                                                                                                            cDNAs, which are differentially expressed in (metastatic)
                                                                                                                                                             Differentially expressed breast cancer associated cDNA #143.
                                                                                                                                                                                   Breast cancer; differential gene expression; BC-cDNA; breast cancer diagnosis; breast cancer monitoring; breast cancer staging; gene; ss.
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                       125 AAACATACAAGACTCCTTCAGCCAAC 150
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                                                                                        ABX77648 standard; cDNA; 1889 BP
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                                                                                                                                      09-APR-2003 (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                       (CHEN/) CHEN H.
                                                                                                                                                                                                                                    Homo sapiens
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         2049
                                                                                                               ABX77648;
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                                                                 RESULT 8
ABX77648
ID ABX7
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20106 AAGATTAGCATGCCCCTGCGCAAGGATGACACGCAAATTCGTGAAGCGTTCCATATTTA 20765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a homozygosity deletion domain co-existing in the 36-position of the first chromosome short arm (1p36) in human neuroblastoma. Also described are base sequences from the 1p36 position of human neuroblastoma call lines (NB-1 and MASS-NB-SCH-1), which are tumour suppressor genes in human neuroblastoma. The genes are tumour suppressor genes in studying mechanism of tumour body formation, and gene diagnosis of tumours as well as in developing anti-cancer drugs. AAF97787 to AAF97829 represent PCR primers used in the exemplification of the present invention, and AAF97810 to AAF97810 represent sequences given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human 1p36 homozygosity deletion domain from the 36-position of first chromosome short arm in human neuroblastoma cell lines, applicable e.g. in gene diagnosis of tumors as well as in developing anti-cancer drugs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; chromosome 1; 1p36; neuroblastoma cell line; NB-1; anticancer;
tumour suppressor; human 1p36 homozygosity deletion domain; tumour;
diagnosis; ds.
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74.1%; Pred. No. 2.4e-12;
tive 0; Mismatches 43;
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2049 AAACATACAAGACTCCTTCAGCCAAC 2074
                                           125 AAACATACAAGACTCCTTCAGCCAAC
                                                                                                                                                                                                                                                                 AAF97854 standard; DNA; 34488 BP.
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09-MAY-2000; 2000JP-0136266.
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Matches 123; Conservative
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Human, immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23092.
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                                                                                                                                                                                                                                                                                                                                                                                        0000US-0198123
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                                 06-NOV-2001 (first entry)
                                                                                                                                                     Homo sapiens
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   AAK68280;
   47552 AAGATTAGCATGGCCCCTGCGCAAGGATGACACGCAAATTCGTGAAGCGTTCCATATTTA 47611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47492 AATAACTAAGCACGGTGCTCGCTTCGGCACACATATACTAAAATTGGAACGATACAGAG 47551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes the coding and protein sequences of the human kinesin-like protein HKLP. It is thought that the protein could be involved in neurological disorders, infertility, spontaneous abortion, neonatal chromosome disorders, aneuploidy and cancers. This is due to its function in the movement of microtubules. The protein shows homology to the murine KIFIA and KIFIB proteins. The sequences disclosed in the invention can be used in the islandation of similar human proteins and in vector production. In addition, the biallelic markers shown can be used in disease diagnosis and population studies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 AAATAGTAATGACTCTGTTTGCTTCAGCAGACATATACTAAAATAGGAGCTATACAAAG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318 AAGATTAGCATGGACTCTGTGCAAGAATGACACAAAATTTGTGAAACATTCCATATATT 377
                                                                                                                                                                                                                Human, kinesin-like protein, HKLP, KIF1, cell division, cancer,
intracellular transport, neurological disorder, infertility,
biallelic marker, spontaneous abortion, neonatal chromosome disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An isolated or purified human kinesin-like protein (HKLP) encoding polynucleotide used to detect HKLP polynucleotides in a sample comprises a contiguous span of at least 12 nucleotides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 121162 BP; 33272 A; 24108 C; 25842 G; 37919 T; 21 other;
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74.1%; Pred. No. 3.6e-12;
Ive 0; Mismatches 43; Indels 0;
                                                                                                                                                                                 Human kinesin-like protein HKLP coding sequence contig SEQ ID
AAAAATAAATAAATAAAGAGAAAAAGGAAAAATTAAAAAGAAA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dufaure-Gare I, Grel P;
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                                                                                 AAC66548 standard; DNA; 121162 BP
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AAK68280
ID AAK68280 standard; DNA; 7141
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Matches 123; Conservative
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                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                     aneuploidy; ds
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08-DEC-2000; 2000US-0251868. 08-DEC-2000; 2000US-0251869. 08-DEC-2000; 2000US-0251999. 11-DEC-2000; 2000US-025990. 11-DEC-2000; 2000US-0259679.

(HUMA-) HUMAN GENOME SCI INC

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2000US-0246528.
2000US-0246532.
2000US-0246609.
2000US-0246610.
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2000US-0246613.
2000US-0249207.
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2000US-0249209.
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2000US-0249211.
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2000US-0249217.
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2000US-0249214
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05-DEC-2000;
06-DEC-2000;
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-NOV-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
amino acid sequences given in AAM8170 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (1)
cytoteins and polynucleotides may be used in the prevention, diagnosis and
cxample, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
cxpression by rectifying mutations or deletions in a patient's genome
cxpression by rectifying mutations of (1). Additionally, (1)
cytoteins and polynucleotides may be used to produce the secreted (1), by inserting
the nucleic acids into a host cell and culturing the cell to express the
cytotein. (1) proteins and polynucleotides may be used to prevent,
c diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
to AAK87694 represent inmune/namatopoietic antigen genomic
c sequences from the present invention. AAK84942 to AAK84950 and AAM82169
represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3982 CCACCACACCTGGCCGTGAACT-TTTTCTTTCCCTTTATTTTCAAAAAAAATGTTTCAT 4040
                                                                                                                                                                                                                                                                                               Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1136 ATATATAGTATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3862 ATTTTTTGTATTTTTAGTAGAATGGGGTTTCACCATGTTGCCCAGGCTAGTTTTGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1196 CCTAAGCT-AAGCAATCTTCCTGTCTTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic sequence #435 encoding for novel human respiratory antigen.
                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 23092; 3071pp + Sequence Listing; English
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Pred. No. 3.3e-12;
0; Mismatches 64; Indels 2;
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                                                                                                                                                                                                                         Ruben SM;
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AAS28595 standard; DNA; 6040 BP
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Best Local Similarity 70.3%;
Matches 156; Conservative
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                                                                                                                                                                                                                      Barash SC,
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10-NOV-2000;
                                                                                                                                                                                                                                                             08-NOV-2000;
anti allergic; anti asthmatic; anti inflammatory; olfactory;
respiratory active; ds.
                                                                                                                                                                                                                                                                                                                                                          14-AUG-2000; 2000US-0226759.
18-AUG-2000; 2000US-0226779.
22-AUG-2000; 2000US-0226779.
22-AUG-2000; 2000US-02267182.
23-AUG-2000; 2000US-0227182.
30-AUG-2000; 2000US-0229149.
01-SEP-2000; 2000US-0229344.
01-SEP-2000; 2000US-0229345.
01-SEP-2000; 2000US-0229345.
01-SEP-2000; 2000US-0229345.
01-SEP-2000; 2000US-0229345.
05-SEP-2000; 2000US-0229345.
06-SEP-2000; 2000US-0239437.
06-SEP-2000; 2000US-0239437.
06-SEP-2000; 2000US-0239431413.
08-SEP-2000; 2000US-02314143.
08-SEP-2000; 2000US-02314144.
08-SEP-2000; 2000US-0231299.
14-SEP-2000; 2000US-0231299.
14-SEP-2000; 2000US-0231299.
14-SEP-2000; 2000US-0231299.
14-SEP-2000; 2000US-0231299.
14-SEP-2000; 2000US-0231299.
14-SEP-2000; 2000US-0231299.
                                                                               17-JAN-2001; 2001WO-US01333
                                            WO200155448-A1
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28-JUN-2000;
30-JUN-2000;
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                                                                                                31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                           Homo sapiens.
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26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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14-AUG-2000;
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14-AUG-2000
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20000S - 023 583 4 20000S - 023 63 46 20000S - 024 64 17 20000S - 024 62 17 20000S - 024 92 18 20000S - 025 10 30 2000S - 025 10 30 2000S

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2000US-0220964.
2000US-0224518.
2000US-0224519.
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2000US-0218290.
2000US-0220963.
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2000US-0231413.
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000US-0225447
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                                                               18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
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14-AUG-2000;
14-AUG-2000;
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07-JUL-2000;
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      The present invention relates to the isolation of novel human respiratory antigens (AAU17685-AAU17975), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing disorders related to the respiratory system including throat disorders e.g. vocal cord paralysis, tonsilities, and laryngitis), ung disorders e.g. pneumonia, allergic disorders e.g. asthma, pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of the invention are useful in gene therapy and antisense therapy. AAS28161-AAS28764 represent genomic sequences encoding for novel to human respiratory antisens.

Change invention are useful in gene therapy and antisense therapy. AAS28161-AAS28764 represent genomic sequences encoding for novel to human respiratory antisens.

Change invention are useful in gene therapy and antisense therapy.

AAS28161-AAS28764 represent genomic sequences encoding for novel to human septiratory antisense.

Change in the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO.

Cat fib.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39455
                                                                                                                                                            Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the respiratory system including respiratory cancers and also for testing and detection e.g. diagnosis -
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                                                                                                                                                                                                                                             Disclosure; SED ID No 1029; 546pp; English
                                                                                  Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK84643 standard; DNA; 4181 BP
                                        (HUMA-) HUMAN GENOME SCI INC.
05-JAN-2001; 2001US-0259678.
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04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0184664.
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Best Local Similarity 72.8°
Matches 123; Conservative
                                                                                                                        WPI; 2001-476224/51.
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                                                                                Rosen CA,
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
cuplement caids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK87690 and AAM82169
represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                          1022 TTCTGACAAGCTCCCACAGGTGATTCCTTTCCCCACAGCATTTGAGAACTTCAGCTCAAT 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3948 TTTTTTTTAGTTGAGACGGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAATGCCTGAT 3889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            4068 TITIGGCTCACIGCAACCTCCGCCTCCTGGGCTTAAGCAATICTCCTGCTTCAGCTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1082 GACCTAATCAGAGTCCTGCCATTGCTAATATCTGGTCTCATTTTTBTCATATATATATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1142 AGTATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAACTCCTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23094.
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Pred. No. 6.6e-12;
1; Mismatches 122; Indels
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04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0184664.
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Best Local Similarity 58.9
Matches 178; Conservative
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                     13-OCT-2000; 2000US-0239335.
13-OCT-2000; 2000US-0239937.
20-OCT-2000; 2000US-024937.
20-OCT-2000; 2000US-0241221.
20-OCT-2000; 2000US-0241786.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-024617.
08-NOV-2000; 2000US-0246474.
08-NOV-2000; 2000US-0246477.
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08-NOV-2000; 2000US-0246523

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17-NOV-2000; 2000US-0249211

17-NOV-2000; 2000US-0249211
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17-NOV-2000; 2000US-0249245.
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17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-024929.
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17-NOV-2000; 2000US-024929.
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2000US - 0186350

2000US - 0199034

2000US - 0199123

2000US - 0199123

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2000US - 0119486

2000US - 011
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2000US-0237039
115-MAR-2000; 116-MAR-2000; 118-MAR-2000; 118-MAR-2000; 118-MAR-2000; 119-MAY-2000; 118-MAY-2000; 11
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08-SEP-2000;
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21.5EP-2000;
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2000US-0239935.
2000US-02319937.
2000US-0241021.
2000US-0241186.
2000US-02411809.
2000US-024181809.
2000US-0244617.
2000US-0244617.
2000US-0246474.
2000US-0246677.
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(HUMA-) HUMAN GENOME SCI INC

S Ruben Barash SC, Rosen CA,

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis metastasis

NO 23094; 3071pp + Sequence Listing; English Disclosure; SEQ ID

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2000US-021436
2000US-0218290.
2000US-0220963.
2000US-0220964.
2000US-0224518.
                                                                                                                         2000US-0225213.
2000US-0225214.
2000US-0225266.
2000US-0225266.
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2000US-0225270.
2000US-0225447.
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2000US-0225759.
2000US-0226279.
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2000US-0229287.
2000US-0229343.
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08-SEP-2000;
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       AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) anno acid sequences given in AAM82170 to AAM91921. (I) have cytostatic amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic certivity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK84942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                               1136 ATATATAGTATTTGTGGTAGAGATGGGATTTTGCCCATGTTGCCCAGGCTAGTATTGAACT 1195
                                                                                                                                                                                                                                                                                                                                                                                   CCTAAGCT-AAGCAATCTTCCTGTCTCTCCCCCAAAATGTTGGGATTACAGGTGTAAG 1254
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cytostatic; gene therapy, vaccine; metastasis; ds.
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69.8%; Pred. No. 7.9e-12;
tive 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                Sequence 7141 BP; 2053 A; 1476 C; 1615 G; 1997 T; 0 other;
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16-MAR-2000; 2000US-0189874.

17-MAR-2000; 2000US-0190076.

18-APR-2000; 2000US-0190176.

19-MAY-2000; 2000US-0205515.

07-JUN-2000; 2000US-0205467.

28-JUN-2000; 2000US-0215135.
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04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0184664.
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Best Local Similarity 69.8
Matches 155; Conservative
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 26249; 3071pp + Sequence Listing; English.

AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with diagnosis expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to
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51170 TAATTTTTGTATTTTTGGTAAAGATGGGGTTTCACCATTTTGGCCAGGCTGGTCTTGAAT 51111
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               polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells, AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169
                                                                                                                                                                                            represent sequences used in the exemplification of the present invention.
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supplement the patients own production of (I). Additionally, (I)
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Pred. No. 1.9e-11;
0; Mismatches 64; Indels 0;
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Best Local Similarity 67.3 Matches 132, Conservative
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Search completed: November 17, 2003, 23:52:55 Job time : 550.27 secs

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Query Match
Best Local Similarity
Matches 118; Conserv
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ORGANISM: Human
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                                                         November 17, 2003, 23:31:50 ; Search time 120.734 Seconds (without alignments) 7582.209 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_coMB.seq:*
/cgn2_6/ptodata/2/ina/bcTuS_COMB.seq:*
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Compugen Ltd
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-09-641-638-200
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US-09-978-197-3

US-09-978-197-3

US-09-671-638-651

US-09-729-995-3

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US-09-67-47-7

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US-09-611-638-199-7

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         version :
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Maximum Match 100%
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        GenCore (c) 1993
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Sequence 3, Application US/09740041

Sequence 3, Application US/09740041

Parent No. 6562593

GENERAL INFORMATION:
APPLICANT MERKULOV, KARI et al
TITLE OF INVENTION: ISCLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO01001

CURRENT APPLICATION NUMBER: US/09/740,041

CURRENT FILING DATE: 2000-12-20

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 66804
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Sequence 5, Application US/09212971B

Sequence 5, Application US/09212971B

Sequence 5, Application US/09212971B

SEQUENCE NO. 6107041

APPLICANT: MacKensluk, Robert G

APPLICANT: Liston, Peter

APPLICANT: Tsang, Benjamin K

APPLICANT: Tsang, Benjamin K

APPLICANT: Pratt, Christine APPLICANT: Title OF INVENTION: DETECTION AND MODULATION OF IAPS AND

TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
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Pred. No. 3.4e-13;
                        4.4%; Scor. 73.3%; Pred. No. 5... 0; Mismatches
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NACHOLIUK, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Liston, Peter
APPLICANT: Tsang, Benjamin K
APPLICANT: Tsang, Benjamin K
APPLICANT: Tsang, Benjamin K
APPLICANT: Trang, Benjamin K
APPLICANT: Peter
APPLICANT: Pasid, Stephen
APPLICANT: Benjamin K
APPLICANT: Pasid, Stephen
APPLICANT: Pasid, 
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4.3%; Score 89.4; DB 4; Length 6669;
Best Local Similarity 73.1%; Pred. No. 7.2e-13;
Matches 128; Conservative 0; Mismatches 46; Indels 1
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4.3%; Score 89.4; DB 3;
Best Local Similarity 73.1%; Pred. No. 7.2e-13;
Matches 128; Conservative 0; Mismatches 46;
PILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bicker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELEPHONE: 617-428-0200
TELEPAX: 617-428-7045
TNEFAX: 617-428-7045
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NAME/KEY: variation
LOCATION: (3677)...(3951)
CTHER INFORMATION: n can be any nucleotide
US-09-617-053A-5
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SEQUENCE CHARACTERISTICS:
LENGTH: 6669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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US-09-617-053A-5
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Sequence 5, Application US/08800929A

Sequence 5, Application US/08800929A

GENERAL INFORMATION:

APPLICANT: MacKenzie, Alexander E

APPLICANT: Baird, Stephen

APPLICANT: Braird, Stephen

APPLICANT: Baird, Stephen

TITLE OF INVENTION: IPPECTION AND MODULATION OF

TITLE OF INVENTION: DISEASE

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
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4.3%; Score 89.4; DB 3; Length 66
Best Local Similarity 73.1%; Pred. No. 7.2e-13;
Matches 128; Conservative 0; Mismatches 46; Indels
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
               TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER FILING DATE: 1996-01-14
EARLIER FILING DATE: 1996-11-14
EARLIER FILING DATE: 1996-11-14
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: variation
CATTON: (3677)...(3951)
COTHER INFORMATION: n can be any nucleotide
VS-09-212-911-5
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FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
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176 Federal Street
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ZIP: 02110
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
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US-08-800-929A-5
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4.2%; Score 87.8; DB 4;
Best Local Similarity 78.1%; Pred. No. 4.2e-12;
Matches 118; Conservative 0; Mismatches 32;
  Pred. No. 4.2e-12;
0; Mismatches 32
                                                                                                                                                                                                                                                                                  11924 GCCACTGCACCTGGCTGGAAGGAGTGATCTT 11954
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  78.1%;
  Best Local Similarity 78.1
Matches 118; Conservative
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ORGANISM: Human
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US-09-641-638-36
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Sequence 1. Application US/09813817

Patent No. 6340583

GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REPERENCE: CLOO1178
CURRENT APPLICATION NUMBER: US/09/813,817
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 59065
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: YAN, Chunhua et al.

ITILE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL001306

CURRENT APPLICATION NUMBER: US/09/984,890

CURRENT FILING DATE: 2001-10-31

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0
                                                               1230 TAATTTTTGTATTTTTAGTAGAGATGGGGTTTTCACCATTTTGGCCAGGCTGGTTTTGAAC 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1090 CAGAGTCCTGCCATTGCTAATATCTGGTCTCATTTTTBTCATATATATATATATG 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1150 TGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAACTCCTAAGCTAAGCAA 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1210 TCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAGCCACTGCACCGGC 1268
                                                                                                                                                     1350 GCCACTGCACCAGGCAGAGGCCTCTTTTTATCTCTTTTTGGCCTCTACAGTG 1404
                                                                                                                            1254 GCCACTGCACCCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTGACCACTCTG 1308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.3%; Score 89.4; DB 4; Length 75395; 72.1%; Pred. No. 1.8e-12; tive 1; Mismatches 48; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1).T.(75395)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                Sequence 3, Application US/09984890
Patent No. 6492156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 72.13
Matches 129; Conservative
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; ORGANISM: Human
US-09-813-817-3
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LENGTH: 75395
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US-09-984-890-3
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RESULT 7

US-09-978-197-3

US-09-978-197-3

Sequence 3; Application US/09978197

Sequence 3; Application US/09978197

Sequence 3; Application US/09978197

Batent No. 6403353

GENERAL INFORMATION:

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

CURRENT APPLICATION NUMBER: US/09/978,197

PRIOR FILING DATE: 2001-10-17

PRIOR FILING DATE: 2001-10-17

SOFTWARE: FASESEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 59065
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Patent No. 6432648

GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFRENCE: GENGET.051CP1
CURRENT APPLICATION NUMBER: US 09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR PRIOR PELING DATE: 2000-02-11
PRIOR FILING DATE: 1999-05-07

PRIOR FILING DATE: 1999-05-07
                                                                                                                  11864 TCCTGACCTCAAGTGATCCACCTGCCTCCGCCTCCCAAAGTGCTGGGATTACAGGGGTGTGA 11923
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                                                                    1135 TATATATATATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAAC
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1; Gaps
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NAME/KEY: allele
LOCATION: 1827
OTHER INFORMATION: 10-510-173 : variable motif ATTA or TTTTT
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OTHER INFORMATION: 10-511-62 : polymorphic base
NAME/KEY: allele
LOCATION: 2323
OTHER INFORMATION: 10-511-337 : insertion of T
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LOCATION: 17555_.20674
COTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 1128
OTHER INFORMATION: 10-508-191 : polymorp
NAME/KEY: allele
LOCATION: 1182
OTHER INFORMATION: 10-508-245 : polymorp
NAME/KEY: allele
LOCATION: 1599
OTHER INFORMATION: 10-509-284 : polymorp
NAME/KEY: allele
LOCATION: 1590
OTHER INFORMATION: 10-509-284 : polymorp
NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION: 16-509-295 : deletion
                                                                                                                                                      OTHER INFORMATION: 5'regulatory region
                                                                                                                                                                       NAME/KEY: exon
LOCATION: 3124..3297
OTHER INFORMATION: exon
LOCATION: 3871..4072
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 5552..5633
OTHER INFORMATION: exon 3
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LOCATION: 12854..13023
DTHER INFORMATION: exon 10
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LOCATION: 16567..16667
OTHER INFORMATION: exon 12
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LOCATION: 16775..16945
OTHER INFORMATION: exon 13
NAME/KEY: exon
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OTHER INFORMATION: exon 11
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OTHER INFORMATION: exon 14
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LOCATION: 12254 .12340
OTHER INFORMATION: exon 9
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LOCATION: 5996..6099
OTHER INFORMATION: exon 5
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LOCATION: 6349..6509
OTHER INFORMATION: exon 6
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OTHER INFORMATION: exon 8
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OTHER INFORMATION: exon 7
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                                                                                                 NAME/KEY: misc_feature
LOCATION: 1123_.3123
                                                    ORGANISM: Homo sapiens
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| Sequence 651, Application US/09641638
| Patent No. 6432648
| GENERAL INFORMATION:
| APPLICANT: Bluemefeld, Marta
| APPLICANT: Bluemefeld, Marta
| APPLICANT: Chumakov, Ilya
| TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS
| TITLE OF INVENTION: BIALLELIC MARKERS DENST: 051CP1
| CURRENT APPLICATION NUMBER: US 09/502,330
| PRIOR PILING DATE: 1999-05-011
| PRIOR PILING DATE: 1999-05-011
| PRIOR FILING DATE: 1999-03-13
| PRIOR FILING DATE: 1999-03-12
| PRIOR FILING DATE: 1999-03-12
| PRIOR FILING DATE: 1999-03-12
| PRIOR FILING DATE: 1999-03-13
| PRIOR FILING DATE: 1999-03-13
| PRIOR FILING DATE: 1999-03-13
| SOFTWARE: Patent.pm
| SEQ ID NO 651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1176 GCCCAGGCTAGTATTGAACTCCTAAGCT-AAGCAATCTTCCTGTCTCTGCCTCCCAAAAT 1234
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                                                                                                                                                                                                                                                               Query Match
4.2%; Score 86.8; DB 4; Length 956;
Best Local Similarity 76.6%; Pred. No. 1.5e-12;
Matches 118; Conservative 1; Mismatches 34; Indels
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PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 36
LENGTH: 956
                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo Sapiens
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OTHER INFORMATION: 10-349-47 : polymorphic base C or T
NAME/KEY: allele
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                                                                    : polymorphic base A or
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                : polymorphic base G or
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                                             LOCATION: 2623
OTHER INFORMATION: 10-512-318
NAME/KEY: Allele
LOCATION: 2832
OTHER INFORMATION: 10-513-250
NAME/KEY: Allele
                                                                                                                                                                                                    LOCATION: 2334
OTHER INFORMATION: 10-513-352 :
NAME/KEY: allele
LOCATION: 2947
OTHER INFORMATION: 10-513-365 :
NAME/KEY: allele
LOCATION: 3802
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NAME/KEY: allele
GOCATION: 6429
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OTHER INFORMATION: 10-347-220
NAME/KEY: allele
                                                                                                                                                     CCATION: 2844
THER INFORMATION: 10-513-262
VAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                            LOCATION: 4062
OTHER INFORMATION: 10-343-231
NAME/KEY: allele
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NAME/KEY: allele
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LOCATION: 6183
OTHER INFORMATION: 10-346-305
NAME/KEY: allele
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NAME/KRY: allele
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OTHER INFORMATION: 10-343-339
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NAME/KEX: allele
CACATION: 6019
OTHER INFORMATION: 10-346-141
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OTHER INFORMATION: 10-346-263
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THER INFORMATION: 10-347-203
AME/KEY: allele
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OTHER INFORMATION: 10-347-271
NAME/KEY: allele
LOCATION: 2341
OTHER INFORMATION: 10-512-36
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NAME/KEY: allele
LOCATION: 4062
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THER INFORMATION:
                                NAME/KEY: allele
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LOCATION: 8608
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THER INFORMATI
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4.2%; Score 86.8; DB 4; Length 20674;
Best Local Similarity 76.6%; Pred. No. Se-12;
Matches 118; Conservative 1; Mismatches 34; Indels 1;
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Patent No. 6399378
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: DANNA T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXPRESSION
FILE REFERENCE: RTS-0207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38; Indels
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                                                             : polymorphic base G or
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OTHER INFORMATION: 10-349-97 : polymorphic base A or
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                                                                                                                        : deletion of CTG
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CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 10
LENGTH: 99500
                                                                                                                                                        LOCATION: 9785

OTHER INFORMATION: 10-349-224 :
NAME/KEX: 311818

LOCATION: 926

OTHER INFORMATION: 10-349-368 :
NAME/KEX: 311818

LOCATION: 12.71

OTHER INFORMATION: 10-350-72 : F
LOCATION: 12.72

OTHER INFORMATION: 10-350-32 :
NAME/KEX: 311818

LOCATION: 3341

OTHER INFORMATION: 10-507-170 :
NAME/KEX: 311818

LOCATION: 3492

OTHER INFORMATION: 10-507-321 :
NAME/KEY: 311818

LOCATION: 33492

OTHER INFORMATION: 10-507-321 :
NAME/KEY: 311818

LOCATION: 3354
              NAME/KEY: allele
LOCATION: 8703
OTHER INFORMATION: 10-349-142
                                                                                                                      OTHER INFORMATION: 10-349-216
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ORGANISM: Homo sapiens
                                                                              NAME/KEY: allele
                                                                                                                                           NAME/KEY: allele
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LOCATION: 13535
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US-09-798-096-10
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US-09-798-096-10
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APPLICANT: Chen, H.
APPLICANT: Chen, H.
ITILE OF INVENTION: MITHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
FILE REPERENCE: 7853-138
CURRENT APPLICATION NUMBER: 08/268,992
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR PILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/106,056
PRIOR APPLICATION NUMBER: 60/106,056
PRIOR FILING DATE: 1998-03-16
PRIOR FILING DATE: 1998-03-16
PRIOR FILING DATE: 1998-03-16
PRIOR PRIOR APPLICATION NUMBER: 60/078,044
PRIOR FILING DATE: 1998-03-16
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4.1%; Score 85.8; DB 4; Length 72604;
Best Local Similarity 72.5%; Pred. No. 1.5e-11;
Matches 111; Conservative 0; Mismatches 42; Indels 0;
                                                                                                                                                                                                                                                                       Length 72604;
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Pred. No. 1.5e-11;
0; Mismatches 42;
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Patent No. 6399762
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LOCATION: all n positions
OTHER INFORMATION: n=a, c, g, or
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Best Local Similarity 72.5%
Matches 111; Conservative
                                                                                                                                        LOCATION: all n positions OTHER INFORMATION: n=a, c,
          TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: modified_base
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ORGANISM: Homo sapiens
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US-09-657-474-7/c
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32753 CCTGACCTCAAGCATTCCACCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAG 32812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: WEI, MING-Hui et al
APPLICANT: WEI, MING-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO0964
CURRENT APPLICATION NUMBER: US/09/729, 995
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                         CCTAAGCT-AAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAG 1254
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US-09-268-992-7/c

Sequence 7, Application US/09268992

Patent No. 6342351

GENERAL INFORMATION:

APPLICANT: Chen, H.

APPLICANT: Chen, H.

APPLICANT: Chen, H.

APPLICANT: Preiner. N.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

TITLE OF INVENTION: AND TREATING CHROMOSOME-18P RELATED DISORDERS

FILE REFERENCE: 7853-138

CURRENT APPLICATION NUMBER: US/09/268,992

CURRENT FILING DATE: 1999-03-05

EARLIER FILING DATE: 1999-01-22

EARLIER FILING DATE: 1998-10-28

EARLIER FILING DATE: 1998-10-28

EARLIER FILING DATE: 1998-06-05

EARLIER FILING DATE: 1998-06-05

EARLIER FILING DATE: 1998-06-05

EARLIER FILING DATE: 1998-06-05

EARLIER FILING DATE: 1998-03-16

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 72604
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                                                                                                                                                                                                                                           CCACTGCACCCGGCTGATAGCTGGTTTCATTTACTCTAT 1293
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Patent No. 6426206
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Best Local Similarity
Matches 104; Conserv
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 3
LENGTH: 29629
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US-09-729-995-3/c
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57460 CCACCACACCCGGCTGTATGAAGCATGTTTTA 57428

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                                                                            GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID WOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLOOL306
CURRENT PILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 3:
LENGTH: 75395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3. Application US/09759359A

Patent No. 6492153

GENERAL INFORMATION:
APPLICANT: RAU-THERIDEH, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THERED MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THERED PROTEINS, AND USES
TITLE REFERENCE: CLOO1043
CURRENT APPLICATION NUMBER: US/09/759,359A
CURRENT PILING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 90541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 75395
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RESULT 14
US-05-984-890-3/c
; Sequence 3, Application US/09984890
; Patent No. 6492156
                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (1).7.(75395)
OTHER INFORMATION: n = A,T,C or G
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Matches 114; Conservative
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Best Local Similarity 76.0
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Human
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US-09-759-359A-3/c
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Db 23114 GGCCAGGCTGCTCAAACTCCTAAGCAATCCACCTTGGCCTTCGCCTCCCAAAGT 230SS
Qy 1235 GTTGGGATTACAGGTGTAAGCCACTGCACCGGC 1268
Db 23054 GCTGGGATTACAGGCGTGAAGCCACTGGCCTGGC 23021
Search completed: November 18, 2003, 07:06:35
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APPLICANT: SCHWARTZ Bertrand
APPLICANT: SCHWARTZ Bertrand
APPLICANT: BRANELEC, Didie.
TITLE OF INVENTION: SEQUENCES UPSTREAM OF THE
TITLE OF INVENTION: THEM AND USES THEREOF
TITLE FEFRENCE: 03806.0530-00000
CURRENT APPLICATION NUMBER: US/10/005,337A
CURRENT FILING DATE: 2001-12-07
PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
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LENGTH: 2074
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                                                  TYPE: DNA
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                                                                                                                                                                   November 17, 2003, 23:33:10 ; Search time 992.544 Seconds (without alignments) 6829.176 Million cell updates/sec
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NUMBER OF SEQ ID NOS: 5
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CORGANISM: Mus musculus
US-10-005-337A-1
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RESULT 3 US-09-974-298-182 , Sequence 182, Application US/09974298 , Patent No. US20020156263A1

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1929 GCGGGAGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATA 1988
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APPLICANT: SHIFFMAN, Dov
APPLICANT: MIKITA, Thomas
APPLICANT: MIKITA, MIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.0%; Score 144.4; DB 10; Length 1889; Best Local Similarity 99.3%; Pred. No. 2.6e-26; Matches 145; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020156263A1 332919.4
NAME/KEY: unsure
LOCATION: 1882
COTHER INFORMATION: a, t, c, g, or other
US-09-974-298-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Incyte ID No. US20030165924A1 332919.4
APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR PILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAACATACAAGACTCCTTCAGCCAAC 2074
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| NAME/KEY: unsure
| LOCATION: 1655-1681, 1882
| OTHER INFORMATION: a, t, c, g, or other
| US-10-240-965-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-240-965-158
; Sequence 158, Application US/10240965
; Publication No. US20030165924A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1889
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LENGTH: 1325
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                                                                                                                                                                                        5 GAGGGAGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCGGCCCCAGCTATATA 64
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                                             Gaps
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Score 144.4; DB 12; Length 1889;
Pred. No. 2.6e-26;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 421, Application US/10252157
; Publication No. US20030190640A1
; GENERAL INFORMATION:
; APPLICANT: Paris, Mary
; APPLICANT: Paris, Mary
; TILLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER;
; TILLE REPERENCE: PA-0027-1 US
; CURRENT APPLICATION NUMBER: US/10/252,157
; CURRENT APPLICATION NUMBER: 60/295,048
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: PERL PROGRAM
; SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030190640A1 332919.4
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APPLICANT: Sharon E. Plon
APPLICANT: Jason M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
FILE REFERENCE: PA-0046 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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LOCATION: 1655-1681, 1882
OTHER INFORMATION: a, t, c, g, or other
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Query Match
Best Local Similarity 99.3%;
Matches 145; Conservative
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APPLICANT: Jed G. Nucht
APPLICANT: Sharon E. Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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US-10-084-817-217
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GENERAL NO. USJOUZUO13958A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ramigaki, Laura Y. (Itc)
APPLICANT: Sibrami, Bradley K.
APPLICANT: Sibrami, Bradley K.
TITLE OF INVENTION: POLYWUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/23,876
CURRENT FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL PROGRAM
SEQ ID NO 5218
LENGTH: 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030119009A1 183198CB1
CURRENT APPLICATION NUMBER: US/10/084,817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure

LOCATION: 1258

; OTHER INFORMATION: a, t, c, g, or other

US-10-084-817-217
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                                               CURRENT FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SOFTWARE: PERL PROGRAM
SEQ ID NO 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Zea mays
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PRIOR APPLICATION NUMBER: 60/220, 964
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-08-14
PRIOR PELICATION NUMBER: 60/220, 964
PRIOR APPLICATION NUMBER: 60/241, 809
PRIOR APPLICATION NUMBER: 60/240, 299
PRIOR PILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/244, 617
PRIOR PILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/244, 617
PRIOR APPLICATION NUMBER: 60/225, 268
PRIOR PILING DATE: 2000-11-01
PRIOR PILING DATE: 2000-09-29
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-29
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-05
PRIOR DATE: 2000-09-05
PRIOR DATE: 2000-0
                             PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: 60/226,757

PRIOR APPLICATION NUMBER: 60/226,868

PRIOR PILING DATE: 2000-08-14

PRIOR PILING DATE: 2000-08-12

PRIOR PELING DATE: 2000-08-16

PRIOR PILING DATE: 2000-08-16

PRIOR PILING DATE: 2000-09-16

PRIOR APPLICATION NUMBER: 60/216,880

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-08-14

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-21

PRIOR FILING DATE: 2000-09-30

PRIOR FILING DATE: 2000-09-30

PRIOR FILING DATE: 2000-08-30

PRIOR FILING DATE: 2000-08-30

PRIOR PILING DATE: 2000-08-30
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APPLICATION NUMBER: 60/237,038
FILING DATE: 2000-10-02
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1136 ATATATAGTATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAACT 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1196 CCTAAGCTAAGCAATCTTCCTGTCTCTCCCCAAAATGTTGGGATTACAGGTGTAAGC 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3357 CCTGACCTCAGCGATCTGCCTGCTCACTCTCAATGTGCTGGATTACAGGCGTGAGC 3298
                                        61 AAGCTGNACCGGTNTGGAGGGCCCAGCAGGGCCAACNCCAGGGANTCCTTCCACGACAG 120
                                                                                                                                                                                                                                                                                                                                                                 Sequence 1029, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICATT ROSEN et al.
; TILLE OF INVENTION: NUMBER: US/09/764,860
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1029
; LENGTH: 6040
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TITLE OF INVENTION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REPERENCE: PC008C1

CURRENT APPLICATION NUMBER: US/10/074,095

CURRENT PELING DATE: 2002-02-14

PRIOR PELING DATE: 2001-01-17

PRIOR PELING DATE: 2001-01-17

PRIOR PELING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

PRIOR PILING DATE: 2000-01-31

PRIOR PILING DATE: 2000-02-8

PRIOR PILING DATE: 2000-02-8

PRIOR PILING DATE: 2000-05-11

PRIOR APPLICATION NUMBER: 60/225,758

PRIOR PILING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 60/225,758

PRIOR PILING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 60/225,758

PRIOR PILING DATE: 2000-07-11

PRIOR PILING DATE: 2000-07-11

PRIOR PILING DATE: 2000-07-16

PRIOR FILING DATE: 2000-07-16

PRIOR FILING DATE: 2000-07-16

PRIOR FILING DATE: 2000-07-11

PRIOR FILING DATE: 2000-07-11

PRIOR FILING DATE: 2000-07-11
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                                                                                                                                      2047 AAAACATACAAGACTCCTTCAGCCAAC 2074
                                                                                                                                                                               121 ANAAACATNCAAGACTCCTTCAGCCAAC 148
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Publication No. US20030077704A1
GENERAL INFORMATION:
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Best Local Similarity 72.8
Matches 123; Conservative
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CORGANISM: Homo sapiens
US-09-764-860-1029
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R APPLICATION NUMBER: 60/227,182
R APPLICATION NUMBER: 60/227,182
R APPLICATION NUMBER: 60/227,182
R APPLICATION NUMBER: 60/225,214
R PILING DATE: 2000-08-14
R PILING DATE: 2000-09-27
R APPLICATION NUMBER: 60/235,836
R PILING DATE: 2000-09-06
R PILING DATE: 2000-09-06
R R PILING DATE: 2000-09-06
R R PILING DATE: 2000-09-06
R PILING DATE: 2000-08-18
R PPLICATION NUMBER: 60/215,135
R R PPLICATION NUMBER: 60/225,266
R FILING DATE: 2000-08-18
R PPLICATION NUMBER: 60/225,266
            R APPLICATION NUMBER: 60/236,802

R FILING DATE: 2000-10-02

R APPLICATION NUMBER: 60/237,037

R FILING DATE: 2000-10-02

R RELING DATE: 2000-10-02

R FILING DATE: 2000-10-02

R FILING DATE: 2000-10-03

R FILING DATE: 2000-10-03

R FILING DATE: 2000-10-03

R FILING DATE: 2000-10-13

R APPLICATION NUMBER: 60/239,935

R APPLICATION NUMBER: 60/239,935

R APPLICATION NUMBER: 60/246,474

R APPLICATION NUMBER: 60/246,474

R APPLICATION NUMBER: 60/246,474

R APPLICATION NUMBER: 60/246,474

R APPLICATION NUMBER: 60/246,532

R APPLICATION NUMBER: 60/246,532

R FILING DATE: 2000-11-08

R FILING DATE: 2000-11-17

R APPLICATION NUMBER: 60/249,210

R FILING DATE: 2000-11-17

R APPLICATION NUMBER: 60/249,210

R APPLICATION NUMBER: 60/225,759

R FILING DATE: 2000-08-14

R APPLICATION NUMBER: 60/225,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFLIGNCE NUMBER: 60/249,208
REPLING DATE: 2000-11-17
RAPPLICATION NUMBER: 60/249,208
RELING DATE: 2000-11-17
RAPPLICATION NUMBER: 60/249,213
REPLING DATE: 2000-11-17
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R FILING DATE: 2000-11-17
R PAPLICATION NUMBER: 60/249,211
R APPLICATION NUMBER: 60/249,211
R APPLICATION NUMBER: 60/249,215
R FILING DATE: 2000-11-17
R APPLICATION NUMBER: 60/249,264
R FILING DATE: 2000-11-17
R APPLICATION NUMBER: 60/249,214
R PILING DATE: 2000-11-17
R APPLICATION NUMBER: 60/249,297
R FILING DATE: 2000-11-17
R FILING DATE: 2000-11-17
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APPLICATION NUMBER: 60/232,081
FILING DATE: 2000-09-08
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1196 CCTAAGCTAAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAGC 1255
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NAME/KEY: misc feature
LOCATION: (1)...(300000)
COTHER INFORMATION: where n may be a or g or c or t/u, unknown or other US-10-262-552-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3417 ATTTTTATTTTTAGTGGAGATGGGGTTTCGCCATATTGGCCAGGCTGGTCTTGAACT
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Publication No. US20030125289A1
GENERAL INFORMATION:
APPLICANT: Gelb, Bruce D.
TITLE OF INVENTION: NOONAN SYNDROME GENE
FILE REFERENCE: 2420/1J859-US1
CURRENT APPLICATION NUMBER: US/10/262,552
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 60/326,532
PRIOR APPLICATION NUMBER: US 60/326,532
PRIOR PILING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3:1
SEQ ID NO 33
LIBNOTH: 300000
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,414
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/233,063
PRIOR APPLICATION NUMBER: 60/232,397
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,401
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
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Query Match Best Local Similarity

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30293 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAGTAGAGATGGGGTTTTGCTATGTTG 30352
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Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITILE OF INVENTION: Polymorphisms in the Human Genome
ITILE OF INVENTION: Polymorphisms in the Human Genome
ITILE OF INVENTION: Polymorphisms in the Human Genome
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-20
PRIOR PILING DATE: 2000-07-20
PRIOR PLICATION NUMBER: US 60/198,676
PRIOR PLICATION NUMBER: US 60/193,483
PRIOR PLICATION NUMBER: US 60/193,483
PRIOR PLICATION NUMBER: US 60/185,218
PRIOR PLICATION NUMBER: US 60/167,363
PRIOR PLICATION NUMBER: US 60/146,002
PRIOR PLICATION NUMBER: US 60/146,002
PRIOR PRIOR DATE: 1999-108-09
PRIOR PLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PRIOR DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-80
PRIOR PLING DATE: 1999-09-80
PRIOR PLING DATE: 1999-09-80
PRIOR PLING DATE: 1999-09-80
PRIOR PLING DATE: 1990-09-80
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                                                                                                                                                                                                                                                                                                                  Query Match
4.5%; Score 93.2; DB 10;
Best Local Similarity 79.2%; Pred. No. 2.2e-12;
Matches 122; Conservative 1; Mismatches 30;
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thes 44;
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                                                                                                                                                                                              OTHER INFORMATION: n equals a,t,g, or US-09-764-877-3933
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Best Local Similarity 73.0
Matches 119; Conservative
                                   LENGTH: 32220
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (9867)
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US-10-027-632-95562
      SEQ ID NO 3933
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                                                                                          35135 GTGCCCAGCCTACATACCTTGGTCTTGACCCTTTTTCCATATTTTTATTTTTATTTTATTTTT 85076
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                                                          1135 TATATATAGTATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAAC
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      1; Gaps
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Publication No. US20030114399A1
Publication No. US20030114399A1
Publicant BLAKELY, RANDY D.
APPLICANT: APPRASUNDARAM, SUBRAMANIAM
APPLICANT: FERGUSON, SHAWN
TITLE OF INVENTION: HUMAN AND MOUSE CHOLINE TRANSPORTER CDNA
FILE REFERENCE: VBLT: 008US
CURRENT APPLICATION NUMBER: US/09/911,077A
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE PATENTIN Ver. 2.1
SEQ ID NO 19
LENGTH: 119040
                                                                                                                                                                                                                                                                                                           1254 GCCACTGCACCCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTG 1299
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Patent No. US20020147140A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
   37; Indels
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Best Local Similarity 66.7%; Pred. No. 3.4e-12;
Matches 134; Conservative . 0; Mismatches 67;
0; Mismatches
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LOCATION: (2347)..(90873)
JOHN INFORMATION: N = A, C, G or T/U
US-09-911-077A-19
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Matches 128; Conservative
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ORGANISM: Homo sapiens
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US-09-911-077A-19/c
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TYPE: DNA
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PRIOR FLING DATE: 2000-03-109

CURRENT FILING DATE: 2002-04-30

PRIOR PAPLICATION NUMBER: US 60/218,006

PRIOR PAPLICATION NUMBER: US 60/218,006

PRIOR PAPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR PILING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-08-08

PRIOR FILING DATE: 1999-09-08-08

PRIOR APPLICATION NUMBER: US 60/146,002
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Sequence 95562, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR PELING DATE: 2000-07-12
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR PELING DATE: 2000-04-20
FRIOR PELING DATE: 2000-04-20
FRIOR PELING DATE: 2000-04-20
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440 TCACTGCATCTGGCCAAATTTCTTGTTTTTTTTTTTT 482
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                          ; Sequence 95563, Application US/10027632; Publication No. US20030204075A9; GENERAL INFORMATION:
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Best Local Similarity 73.0
Matches 119; Conservative
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US-10-027-632-95562
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Pred. No. 2.6e-13;
0; Mismatches 44;
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 95562
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 73.0%;
Matches 119; Conservative
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US-10-027-632-95562
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CD244827 AGENCOURT AQ207760 HS 3026 B AA494075 ng61c08.5 AA917468 ol51f11.9 BC038630 Homo sapi AI039619 ox28f05.x

OM nucleic

Run on:

Sequence:

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AQ480395 10-236B22.TV RPCI-11 Homo sapiens genomic clone RPCI-11-236B22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 522)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other GSSs: RPCI-11-236B22.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC

    (Dases 1 to 522)
    Abao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and J.C.

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BY079997
AQS84830
CDG48530
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AA994075
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BC038630
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AZ295534 RPCI-23-1
AU139209 AU139209
BY091041 BY091041
                                                       2003, 23:31:10 , Search time 4326.29 Seconds (without alignments) 11651.427 Million cell updates/sec
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       version :
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Maximum Match 100%
Listing first 45 summaries
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T39841 yal1c09.r3 AQ895064 HS 3175 A CD520493 AGENCOURT AI288531 q191a04.x

BF738217 CM3-KT003 BF829139 MR1-HN007 AZ335882 110-C6512 BF415552 U1-R-CA1-BZ260574 CH230-285 AZ4060305 1M0175C06 AA947380 cd86606 y BF724783 bx08f06 y BF400140 U1-R-CA1-AQ187593 HS 3132 A BG390793 G02416657 AQ10862 CTT-HSP-2 AQ468422 nC76707. y BG390793 G02416521 AQ19900 HS 3252 A AZ355944 HMG12211-12 AQ219900 HS 3252 A AZ355940 HOMO SAD1 AU720761 AV720761 AV720761 AV720761 AV720761 AV720761 AV7207651 AV720761 AV720765 AV720761 AV720765 AV720761 AV720765 AV720761 BE791763 G0221956 BF791763 G0221956

Minimum DB Maximum DB

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Searched:

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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Mus musculus genomic clone RPCI-23-105P3,
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library availability please contact Pieter de Jong pleterAdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.class: BAC ends.
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                                                                                                                                                                                                                                                                                 /cell type="Lymphocytes"
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/note="Vector: pBACe3.6; Site_l: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
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Pred. No. 2.5e-19;
1; Mismatches 5; Indels
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                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                      /mol_type="genomic_DNA"
/db_xref="GDB:7590285"
/db_xref="taxon:9606"
/clone="RPCI-11-236B22"
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Mus musculus (house mouse)

genomic survey sequence AZ295534.1 GI:9537319

AZ295534

ACCESSION VERSION

GSS

KEYWORDS SOURCE ORGANISM

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/sex="remaic
/lab.host="Dhlos"
/lab.host="Dhlos"
/clone lib="RPCT-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female CSTBL/6J mouse kidney and/or
brain genomic DNA was isolated and partially disested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
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                                                                                                                                                               Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: szhaogeigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 105 row: P column: 3
Seq primer: SP6
Class: BAC ends.
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                                                           Rodentia; Sciurognathi; Muridae; Murinae; Mus
Chordata; Craniata; Vertebrata; Euteleostomi;
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Other GSS: RPCT-23-105P3.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Fax: 301 838 0200
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="RPCI-23-105P3"
/sex="Female"
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Mus musculus (house mouse)
Mus musculus
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Fax: 81-45-503-9216
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 1834 AGCAGGTTAGCTTGTCCTCCCTCCTCTTTCAGCTTCCCAGACACTGAGTTGGAATGA 1893
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                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 735)
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genomics@hri.co.jp
HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                 374 GGAATGAAATTCACCTGCTCTGAATTGGCCACTGGTGGGGGGCAGGGTGTGACTTGGC
                                                                       TTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGG
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Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 241; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
122-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
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/db_xref="taxon:9606"
/clone="PLACE1010155"
/tissue type="placenta"
/clone_lib="PLACE1"
/note="Vector: pME18SFL3"
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AU139209.1 GI:11000730
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BY079997 RIKEN full-length enriched, 10 days neonate heart Mus musculus cDNA clone K630022E19 5', mRNA sequence.
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Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Salto,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yaqi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Bradt,D., Brusic,V., Chothia,C., Corbani, L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest
                                         encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 AGACACTAAGTCTGGAATGAAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGGCAGG 179
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/dev_stage="10 days neonate"
/dlone_lib="RIKEN full-length enriched, 10 days neonate
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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Computer-based methods for the mouse full-length cDNA
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81.3%; Pred. No. 0.012;
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Normalization and subtraction of cap-trapper selected CDNAs to prepare full-length CDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2011)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Croup in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computational Analysis of Full-Length Mouse cDNAs Compared with
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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Score 158.4; DB 13; Length 353; Pred. No. 0.27;

7.6%;

Query Match Best Local Similarity

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205

145

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="lwater" | Adote = 10376302"

/tissue_type="White Matter" |
/dev_stage="Unknown" | A T1 and T5 phage resistances)"

/clone lib="NIH MGC 181"

/clone lib="NIH MGC 181"

/clone lib="NOW-SPORT6.1; Site_1: NotI; Site_2: ECORV (destroyed); Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1:42 kb. Library was constructed by linear taxe 1:42 kb. Library was constructed by linear this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                1215 CTGTCTCTCCCCCAAAATGTTGGGATTACAGGTGTAAGCCACTGCACCCGGCTGATAG 1274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 827)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                                                                                                                                             204 CTGCATCGGTCTCCCCAAAGTGCTGGGATTACAGGTGTGAGCCACTGCACCTGGCCCATAT
                                                                                                                                              1096 CCTGCCATTGCTAATATCTGGTCTCATTTTTBTCATATATATATATATATATTGTGTAG
                                                                                                                                                                                         324 CATGCCCAGCTAAAGATCAGATATCCTTTTTATAATTTTTTTATTGTATTTTTGGTAG
                                                                                                                                                                                                                                       1156 AGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAACTCCTAAGCT-AAGCAATCTTC
                                                                                                                                                                                                                                                                                  264 AGACAGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAACTCCTGACCTCAAATGATGTCTGC
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Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information clond through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: NDAM418 row: 1 column: 07
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AGENCOURT 14096429 NIH_MGC_181 Homo sapiens cDNA clone
IMAGE:30376302 5', mRNA sequence.
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Pred. No. 5.5e+02;
0; Mismatches 44; Indels 0
                                                       Length 343;
                                                                                                  Indels
                                                     Score 98.6; DB 28;
Pred. No. 9.6e+02;
                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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                                                     Query Match
Best Local Similarity 72.1%;
Matches 142; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343 bp DNA linear GSS 07-JUN-1999
Homo sapiens genomic clone RPCI-11-456H3,
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                                                                                                                                         CTTCCCAGACACTGAGTCTGGAATGAAATTCACCTGCCTCTGAGTTGGCTCCTAATGGG 1927
                                                                                                                                                                                                                                                                                                                              1928 GGCGGGAGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATAT 1987
                                                                                                                                                                                                                                                                                                                                                                                                                       62 CACATTTCTTCCTGATTCGNATACGCCGCGG----NCAGCTTGTCATCTCCCTCTTGGG 116
                                                                                                                                                                                                                                                               234 TAACGGGCTGTGTGGAGGGCTCCACAGGCCAGTTCAGGGGTTCATCCACAAGAGAGA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from ASPPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.Seq primer: T7
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 343)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
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/clone_lib="RPGT-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
                                                                                              2 GATACGIGGGATGACICGCATIGCTGAGCGTGIGGTCACIGCCAAAGGAAIGACCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                         177 GGCAGGGGTGTGACTTGGCTTCCCAGGCTGGAAG---ATATCTCACCAGCCCTACTAA
                                                1748 GACAAATAGGATGACTTGCATTGCTGAGCGATGTGATCACCACCAAAGGAATGGCCCTCT
       Gaps
       8
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Contact: Shaying Zhao, William Nierman, Mark Adams
       73; Indels
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/db_xref="GDB:7674890"
/db_xref="taxon:9606"
/clone="RPCI-11-456H3"
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CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 841 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 408.
                                                                                                                                                                              AA494075 412 bp mRNA linear EST 19-AUG-1997 ng61c08.s1 NCI CGAP_Lip2 Homo sapiens cDNA clone IMAGE:939278 similar to contains Alu repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="liposarcoma"
/lab_host="DHIOB"
/clone_lib="NCI_CGAP_Lip2"
/clone_lib="NCI_CGAP_Lip2"
/note="Vector: pAMPI0; mRNA made from liposarcoma, cDNA made by oligo-dT priming. Non-directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
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                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I ( bases 1 to 412) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1189 TIGAACTCCTAAGCTAAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGG
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Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 412;
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Pred. No. 1.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
/clone="IMAGE:939278"
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82 c 13
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AA494075.1 GI:2223916
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Best Local Similarity 74.8%;
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                           1314 TTTTGAAGTAAA 1325
                                                                    471 TTGCAACATAAA 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished
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AA494075/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 502)
Mahairas G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                AQ207760 502 bp DNA linear GSS 18-SEP-1998 HS_3026_B1_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=19 Row=N, genomic survey
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                                                                    AAGATTAGCATGGACTCTGTGCAAGAATGACACACAAATTTGTGAAACATTCCATATATT 377
                                                                                                             522 AAGATTAGCATGGCCCCTGCGCAAGGATGACACGCAAATTCGTGAAGCGTTCCATATTTA 463
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
B-Coli DH10B"
1 117 c 110 q 140 t
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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                                                                                                                                                                                                     High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
TEL: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
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|mol_type="genomic DNA"
|AD_xref="taxon:9606"
|clone="plate=3026 Col=19 Row=N"
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Plate: 3026 row: N column: 19
Class: BAC ends
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Location/Qualifiers
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/lab_host=="URAGE:1527021"
/lab_host="DH10B"
/clone="IntAGE:1527021"
/clone="Organ: pooled; Vector: p7773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and se circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731339. Subtraction by Bento Soares, and M. Fatima Bonaldo. "
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Homo sapiens, Similar to hypothetical protein FLJ20489, clone
IMAGE:5263792, mRNA.
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                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bamanlai; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 464)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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ol51f11.sl Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:1527021 3' Similar to SW:TSG6 HUMAN P98066 TUMOR NECROSIS
FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR ; contains Alu repetitive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL , contact the IMAGE Consortium (infc@image.llnl.gov) for further information. Insert Length: 417 Ed Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 345.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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Homo sapiens
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 73 Row: i Column: 4 This clone has the following problem: retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A1039619 315 bp mRNA linear EST 30-JUN-1998 ox28f05.x1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:1657665 3' similar to WP:T20D3.3 CE03672 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1129 CATATATATATATAGTATTTGTGGTAGAGATGGGATTTTGCCCATGTTGCCCAGGCTAGTA 1188
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2772)
                                                                                                                              Direct Submission
Submitted (15-007-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                            USH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: capabs-rémail.nih.gov
Tissue Procurement: Milos Palkovits, M.D., Ph.D.
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadandssystemsbiology.org
contact: amadandssystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anuradha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1057 TTCAACTCCTGACCTCAGGTGAACTTCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGG
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68.9%; Pred. No. 4.8e+02;
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623 c 602 g 865 t
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                                                                                                    Strausberg, R.
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                                                                                                                                                                                                                            Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
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1 (Dases I to 369)

1 (Dases I to 369)

1 (Dases I, Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare Simpson,A.J.
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mRNA sequence.
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 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                 Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 296.
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CM3-KT0033-151200-572-£07 KT0033 Homo sapiens CDNA,
BF738217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 93.8; DB 9;
Pred. No. 1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                Location/Qualifiers
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10737800
Contact: Simpson A.J.G.
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Best Local Similarity 72.2%;
Matches 122; Conservative
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                                    Tumor Gene Index
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ORGANISM
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AUTHORS
TITLE
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VERSION
KEYWORDS
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AUTHORS
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PUBMED
COMMENT
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BF738217
                                                     JOURNAL
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="mRNA"
/db_xref="mRNA"
/db_xref="mrans.ps66"
/dev_sref="mrans.ps66"
/dev_stage="Adult"
/clone_lib="kT0033"
/clone_lib="kT0033"
/note="forgan: bladder tumor; Vector: pucl8; Site_l: Smal;
/note="forgan: bladder tumor; Vector: pucl8; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning-products
Site_2: Smal; A mini-library was made by cloning-products
Gerived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles:into the pUC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                               Fax: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL

Froject. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3.KT0033-
151200-572-f07&t3=2000-12-15&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 15

High quality sequence store: 369.
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BR8129139 GI:12174344
EST.
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1 (bases 1 to 4 arcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Bruntein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1195 TCCTAAGCTAAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAG 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1255 CCACTGCACCCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTGACCACTCTGATCCAT 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 TAATITITGIATITITGGTAAAGAIGGGGTITICACCAITITITGGCCAGGCTGGICTIGAAT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 TCACTACACCCAGCCTTTAGATTTGTGTAGAGTACATTCTATGAGGTTCACACAATGATGA 258
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 93.6; DB 10;
Pred. No. 1.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
4.5%; Score 93.6; D
Best Local Similarity 67.3%; Pred. No. 1.8e
Matches 132; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1315 TTTGAAGTAAAATGC 1330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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E., SLC, UT

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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="wouse 10kb plasmid UUGCIM library"
/note="Westor: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oilgonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb zange using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 AGATGAAGAGCCAATGAAAATAGTAATGACTCTGTTTGCTTCAGCAGGACATATACTAA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              530 AGACAAAGCACATAATTANAAATGAGAGTACTGTGCTCGCTTCGGCAGCACATATACTAA
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                                                                                                                                                      Biomedical Polymers Research Bldg., 20 S. 2030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0065 row: G column: 12
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: November 18, 2003, 07:01:59 Job time : 4336.79 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .723
/organism="Mus musculus"
                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                             Class: plasmid ends
High quality sequence stop: 723.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="UUGC1M0065G12"
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Best Local Similarity 71.18
Matches 123; Conservative
                                                                                                                                                      Rm. 308, Bi
84112, USA
                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Site 2: Smal, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                            Email: asimpsonouldwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR1&t2=MR1-HN0070-151200-003-h04&t3=2000-12-15&t4=1)
High quality sequence stop: 464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1071 TTCAGCTCAATGACCTAATCAGAGTCCTGCCATTGCTAATATCTGGTCTCATTTTTBTCA 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1131 TATATATATATAGTATTTGTGGTAGAGATGGGGATTTTGCCATGTTGCCCAGGCTAGTATT 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1191 GAACTCCTAAGCT-AAGCAATCTTCCTGTCTTGCCTCCCAAAATGTTGGGATTACAGGT 1249
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1 (Dases 1 to 723)
2 (Dann, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev stage="Adult"
/clone lib="HN0070"
/note="Organ: head_normal; Vector: puc18; Site_1: Smal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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low stringency cona
îr ^ 145 g
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                                                                                                                                                                                                           Tel: +55-11-2704922
Fax: +55-11-2707001
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AUTHORS
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359 589

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649

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Run on:

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DEFINITION
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AUTHORS
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AX468603
LOCUS
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5.1.6
Compugen Ltd.
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version 5
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Maximum Match 100%
Listing first 45 summaries
                                          - nucleic search, using sw model
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GenCore (c) 1993
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AX468604 Sequence
AF111884 Homo sapi
AL590622 Human DNA
AX322775 Sequence
BD094076 Shear str
X83703 H.sapiens m
G28603 human STS S
AC074094 Homo sapi
AC122467 Mus muscu
AC122467 Mus muscu
AC122505 Mus muscu
AC122267 Mus muscu
AC12267 Mus muscu
AC122676 Mus muscu
AC13697 Rattus no
AL172285 Mouse DNA
AL6620467 Mus muscu
AC122676 Mouse DNA
AL662068 Mouse DNA
AL662068 Mouse DNA
AL662068 Mouse DNA AX468603 Sequence AC119234 Mus muscu AC105469 Rattus no AC097115 Rattus no BV062893 S21226025 AF478692 Mus muscu BV076484 S2122F6036 AL772175 Mus muscu AC128695 Rattus no AC128045 Rattus no AC123610 Mus muscu AC105665 Rattus no AC128995 Rattus no AC108661 Rattus no AC109696 Rattus no AC109696 Rattus no AC108661 Rattus no AC113514 Mus muscu AC114128 Mus muscu AC124423 Mus muscu AC124423 Mus muscu AC123396 Mus muscu AC123396 Mus muscu AC123396 Mus muscu AC13396 Mus muscu AC13396 Mus muscu PAT 16-JUL-2002 Mus musculus Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus Schwartz, B., Branellec, D. and Chien, K. Sequences upstream of the carp gene, vectors containing them and uses thereof score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description linear DNA ALIGNMENTS 2358 bp Sequence 1 from Patent WO0246220. AX468603 AX468603.1 GI:21901402 SUMMARIES AX322775 BD094076 HSRNACINP AC132348 AC102022 AC122205 AL365434 AF131883 AL365324 AL772285 AC091467 AC105469 AC097115 BV062893 AF478692 AC022675 AC119697 AX468603 AC119234 AC122467 AC094069 AC108661 AL663088 AC109696 AC116128 Mus musculus (house mouse) 1070 9 9 2 2 55121 DB 5.1 184754 5.1 184754 5.0 234469 5.0 153899 5.0 227165 5.0 243290 5.0 243290 4.9 177706 4.9 231573 Length .5 1901 .5 1901 .5 1901 .4 160350 .3 110480 4.9 245489 4.9 240006 4.9 167223 4.9 219619 4.9 244328 4.9 183205 229640 238344 100.0 97.6 37.3 37.3 Query Match 1 Score 119.6

Db 841 CTTGTCACTTCAAGAGGTCAAAGAAAATAGTGTTAACCATGAAAAGGAGAAGACCAACAG 900	901 TTATCCATTGATAGGCTCTCAGGACAGATAGGACAGAGAAGAGAAGAGGAAGGGAACC 96 901 TTATCCATTGATAGCTCTCAGGACAGATAGGACAGAAGAAACC 96	aaggacaaggtat aaggacaaggtat	1021 AGAAACACAATTTGCTGGTTGAACAGCTGAAGTGGGGGGTGGGGGTTCTTACCCCATGTTCA 	1081 TGGAAGGGTGAGTGAGAGAGAGATATATGATGGCCAGCATAACAAACA	OY 1141 CCCTAATTAACACTTCCCTCTTCTACTGACACCCCTTCACTCTCTCT	1201 TAAAAAAGTATTTTATGTGGCTCTTACGATAGAATCTTTCCTCGAACTATAAAAGATC 12 	1261 TAAATATTTATATTTTTCACATTTTAATATCTTAGGGATGACAAGCAGAACAAGTATT 13 	1321 TTTGCCTCTCTCAAAGCAAAGCTTGGGGCCTTTTTGTTTCGTGTTAGGAATAGAACA 1	1381 CGAGAGCCCCGTGTATCTAGGCAGATGCTCTATCATTAGCCCATGAGTCTCCAGCCTCAG 1	Qy 1441 ACGCACATTTTCTCGGGCTCTTTAAGCTTTTCCCACAGCATTGGGAAACTTTACTGAC 1500 1441 ACGCACATTTTCTCGGGCTCTTTAAGCTTTTCCCACAGCATTGGGAAACTTTACTGAC 1500	1501 AGCATCCAAGTTGTGCTTCTGCTAAGAACTGGACTCACATCTCTGTGCATCACTTCGG 1		OY 1621 GCACTAATTATGGCCAGTGACACCATAGAGTCAAAGTGCATTACTGAATGCTTTCAATTT 1680 1621 GCACTAATTATGGCCAGTGACACCATAGAGTCAAAGTGCATTACTGAATGTTCAATTT 1680	OY 1681 CTCCTAATGCTGGTACGATGGCATGTCACAGGCCATTTTAGCTGCAGACATCACTCCAG 1740	1741 AGAATTCCAAACAGATAGAGACAAGTGGCACCCAGCCCATCTCCTTCCCTCGGGCTGA 180 1741 AGAATTCCAAACAGATAGAGACAAGTGGCACCCAGACCCATCTCCTTCGGGCTGA 180	Qy 1801 TTATCCCCAGAATAGGATGTCCCAAAGCAACACTTCCCAGCCAACTGGAGTGCTGATAA 1860	OY 1861 GTCCAGTTATCAGAAAGATATGGCTGTAAGTGTGATGCACAGTGCTTGCATTTTCTTGAT 1920	OY 1921 ACGTTAGTCATATGAGAGCTGACAAAGAGAAAAAAGAGCAGCGATGTGGTGCAATATTA 1980 1921 ACGTTAGTCATATGAGAGCTGACAAAGAAGGAAAAAAGGCGGTGGTGCGTGC
JOURNAL Patent: WO 0246220-A 1 13-JUN-2002;	Aventis Pharma S.A. (FR California at San Diego Location/Quali ce 1. 2358	/organism="Mus musculus" /mol_type="genomic DNA" /mol_type="genomic DNA" /mol_type="genomic DNA" /mol_type="laxon:1000" BASE COUNT 636 a 567 c 542 g 613 t	tch al Simila: 2358; Co	AATATCAACCCTAACCCAAGGGAACAGCCTGCCTGACGT 60	Qy 61 GGCTTTGCCACCCATGAATACTTCCTAGTCCTTTGTGAAACTCAGCCCATCCCA 120 Db 61 GGCTTTGCCACCCATGAATACTTCCTAGTCCTTTGTGAAACTCAGCCCATCCCA 120	10101 	TTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGGCCTCGACCCCTTTGG	Qy 241 GGGAATCAAACGACCCTTTACAGGGGTCACATATCATCTATCT	CATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTAT 3 	361 GATTGAAGGTCACCACAACATGAGGCCGCCACACTGTTCTAGAGAAAAATCACCTGGGTG 4	421 GGGAAAGGTTTGGGAAAGCCTTTCTGTCTTCATCTTCATCATCGTGTGTGT	GAAAGCCTTTCAGCTGTTCTGGTGGGGCTCTTAGTAGTCTGAGTAGGAACTGTATGTA	541 CAGGTCTGCTTCTTATGGGTGGAGCCAAGACGCATGGTGGGTG	601 CACCTICTAGCICTGCATCCATAGCAAGTAGCCTAATGTTTCTGTGTCTAGGTGTCATCT	661 CTGTGAATCGAGATCCTTGGCTTGATTAGGGAGCCAAAAAAAA	Qy 721 AAGACTGCTCAGCCCAGAGTCCTTCAAAGGAAAGGTCTCAAACCCCCC 780 Db 721 AAGACTGCTCAAGGAATCCTTCCTCAAAGGAAAGGAAAG	781 TTAGCTCTGAGTCAGGCCTGGAACAACGGCCACAGGAATGAGAAAAGCTGCCATAGCTG 84 [841 CTTGTCACTTCAAGAGGTCAAAGAAATAGTGTTAACCATGAAAACGAGAAGAACAACAG 90

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Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Allen, N., Alachchi, H.M., Barna, N., Bastien, V., Anderson, S., Arachchi, H.M., Caoke, P., Corum, B., Chang, J., Choopel, Y., Collymore, A., Cooke, P., Coven, B., Carachlano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Firzderald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand, P., Kalls, K., Dorris, L., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Indblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., Mcactrhy, M., Meldrim, J., Meneus, L., Minon, T., Mahders, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Schawan, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Schawan, S., Severy, P., Smith, C., Vassillev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wassillev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Vassillev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Viell, W., Volmig, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

Ill, 2003 this sequence version replaced gi:31455706.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp:genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* Gills: Gaps of 100 bp

* 61127 142902: Contig of 81676 bp in length.
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Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
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/db_xref="taxon:10090"
/clone="RP94-211P24"
/clone lib="RP01:24 Male Mouse BAC"
41376 a 30899 c 29987 g 40473 t 167 (
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99.9%; Pred. No. 0;
cive 0; Mismatches
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ORIGIN
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JOURNAL
AUTHORS
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                                                                                                1981 ACAGGCAGCTGTCCCCTGGCTTCCCGATACGTGGGATGACTCGCATTGCTGAGCGGTGTG 2040
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Mus musculus clone RP24-211P24, *** SEQUENCING IN PROGRESS ***, 2
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 142902)
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                                                                                                                                                                                                                  2101 CTTGTCATCTCCCTCTTGGGCTTCCCCAGACACTAAGTCTGGAATGAAAATTCACCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2161 CTGAATTGGCCACTGGTGGGGGGGGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATC
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                                                                                                                                                                         GTCACTGCCAAAGGAATGACCCTCTCACATTTCTTCCTGATTCGCATACGCCGCGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGAATTGGCCACTGGTGGGGGGCAGGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATC
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HTG; HTGS PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
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DEFINITION
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Library Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA
ON NOV 15, 2002 this sequence version replaced gi:23101653.
The sequence in this sequence version replaced gi:23101653.
The sequence in this assembly is a combination of BAC based reads and whole genome shockyun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole senome shockun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: Phrap; version 0.990329
Consensus quality: 215126 bases at least Q40
Consensus quality: 217436 bases at least Q20
Consensus quality: 218866 bases at least Q20
Estimated insert size: 214300; sum-of-contigs estimation
Quality coverage: 10x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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215567: gap of unknown length
218782: contig of 3215 bp in length
218882: gap of unknown length
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220459: gap of unknown length
221614: contig of 1155 bp in length
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228280: gap of unknown length
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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225986: gap of unknown len
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224871: gap of unver
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Center clone name: CH230-140I18
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clone_end:T7"
complement(7251..8156)
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/db_xref="taxon:10116"
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                                                                                                                        COMMENT
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                                                          AC105469 229640 bp DNA linear HTG 15-NOV-2002 Rattus norvegicus clone CH230-140118, WORKING DRAFT SEQUENCE, 9
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                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                             AC105469.4 GI:25007338
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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Direct Submission
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*** SEQUENCING IN PROGRESS ***,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                      1629 TATGGCCAGTGACACCATAGAGTCAAAGTGCATTACTGAATGCTTTCAATTTCTCCCTAAT
                                                     141521 TATGGCCAGTGACACCATAAAGTAAAAGTGCATTACTGAATGCTTTCAATTTCTCATAAT
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus
Rattus norvegicus
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0; Mismatches 177; Indels
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Best Local Similarity 82.3%;
Matches 1209; Conservative
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Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Dragan, Dragan, Dragan, Dragan, Dragan, Dragan, Dragan, Baves, K., Bagan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fani, G., Franser, C.M., Garza, M., Garcia, A., Garcia, A., Garcia, A., Garcia, A., Garcia, M., Harles, S., Haldun, S.L., Hodgon, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Scott, J., Liu, W., Liu, Y., Levon, J., Levis, L., Li, L., Liu, J., Liu, J., Liu, M., Liu, Y., Lebow, H., Levan, J., Levis, L., Li, J., Liu, J., Liu, M., Mahindartne, M., Martin, R., Martin, R.,
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Direct Submission

Submitted (11-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (Dases 1 to 238344)

Rat Genome Sequencing Consortium.
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AUTHORS
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TITLE
JOURNAL
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TITLE JOURNAL

REFERENCE

COMMENT

Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu

Center: Baylor College of Medicine

Center code: BCM

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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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                                                                                      Consensus quality: 222569 bases at least Q40 Consensus quality: 226638 bases at least Q30 Consensus quality: 229427 bases at least Q30 Estimated insert size: 233018; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26478 ----CACTAGGAGAGAGAAACCCACGAAGGA-----TATCAGTGTGGTGGTTTCCAGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 879.8; DB 2; Length 238344;
Pred. No. 1e-245;
0; Mismatches 177; Indels 83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236546: contig of 236546 bp in length 236646: gap of unknown length 238344: contig of 1698 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6855 others
                   Center clone name: CH230-26A2
------ Summary Statistics
Assembly program: Phrap, version 0.990329
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63454 a 47381 c 49225 g 71429 t
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/db_xref="taxon:10116"
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Center project name: GGQJ
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BV062893 838 bp DNA linear STS 31-MAY-2003 S212P60252FC3.T0 CZECHII/Ei Mus musculus STS genomic, sequence tagged site.

BV062893.1 GI:31178688

BV062893/c DEFINITION ACCESSION VERSION

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                                                                                                                                                                                Wade, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C. Lander, E.S., Lindblad-Toh, K. and Daly, M.J.
The mosaic structure of variation in the laboratory mouse genome Nature 420 (6915), 574-578 (2002)
                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 838)
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310 Charles Street, Cambridge, MA
Tel: 6172521477
Fax: 6172580903
Email: Kerseli@genome.wi.mit.edu
Primer A. None
                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kerstin Lindblad-Toh
Mus musculus (house mouse)
Mus musculus
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Best Local S:
Matches 831
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TCTCCTTCCCCTCGGGCTGATTATCCCCAGAAATAGGATGTCCCAAAGCAACACTTCCCA 1840
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 665)
Wade, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C.,
Lander, E.S., Lindblad-Toh, K. and Daly, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                      61 TTACTGAATGCTTTCAATTCTCCTAATGCTGGTACGATGCCATGTCACAGGCCCATTTT 120
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S212RF6369FF7.TO CZECHII/Ei Mus musculus STS genomic, sequence
tagged site.
BV076484
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                                                                                                                                                                                                    5,
                                                                                                                                              10; Length 723;
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                                                                                                                                              Score 646.2; DB 10;
Pred. No. 1.5e-177;
0; Mismatches 13;
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           /db_xref="GI:19110907"
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                                     /translation="M"
185 c 180
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Best Local Similarity 97.5%;
Matches 699; Conservative
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
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AUTHORS
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                                                                                                                                                                                         אני ארס 10-OCT-2002 הנייא שמנים אוני מארס מאנים מארס 10-OCT-2002 שנו שואס שונים אונים מארס מארס מארס מארס מארס בריביה אינים א
                                                                                     TGAGTCTCCAGCCTCAGACGCACATTTTTCTCGGGCTCTTTAAGCTTTTCCCACAGCAT 1483
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1 (bases 1 to 723)
Maeda_T., Sepulveda,J., Chen,H.H. and Stewart,A.F.R.

alphal-Adrenergic activation of the cardiac ankyrin repeat protein
gene in cardiac myocytes
Gene 297 (1-2), 1-9 (2002)

2 (bases 1 to 723)
                                     421
                                                                                                               420 TGAGTCTCCAGCCTCAGACGCACATTTTTCTCGGGCTCTCTTAAGCTTTCCCCACAGCAT 361
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300 TCTGTGCATCACTTCGGCCCGTTTTGGGGTAGATCCTCTGATTAGCCTTCAGATTAGAA
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Macda,T., Sepulveda,J. and Stewart,A.F.R.
Macda,T., Sepulveda,J. and Stewart,A.F.R.
Direct Submission
Submitted (29-JAN-2002) Cardiovascular Institute, University
Fittsburgh, 200 Lothrop Street, Pittsburgh, PA 15213, USA
Location/Qualifiers
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|product="cardiac_ankyrin_repeat_protein"
|protein_id="AAL85342.1"
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="FVB"
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1. .>723
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Mus musculus
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AF478692.1 GI:19110906
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/gene="Carp"
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/gene="Carp"
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/gene="Carp"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                     1642 TGTAGGGCATCTACATTTTCTTGATA-GGTAGTCATATGAAAGCTGACAAAGAA--AAAA
 CTCGTTCTGAAGGTTCTAGAAACACAATTTGCTGGTTGAACAGCTGAAGTGGGGGGTGGGG
                                                     1289 TCTATTTCTTGACCACTCTGATCCATTTTGAAGTAAAAATGCTCCAATTATTATGCTGTT
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                                                                     1466 TTTAGC-CCAGACATCACTCCAAAGAATTCCAAACAGATATAGACAAGATATAGGGC
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Sequences upstream of the carp gene, vectors containing them uses thereof
Patent: WO 0246220-A 2 13-UN-2002;
Aventis Pharma S.A. (FR); The Regents of The University of California at San Diego (US); Benoit, Patrick (FR)
Location/Qualifiers
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Pred. No. 5.9e-96;
0; Mismatches 162; Indels
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Best Local Similarity 76.4%;
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                                                                                                                                                                                                                                                                                                                                                                                         sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                      as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the Strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.
                                                                                                                                                                                                                                                                                      were generated from 129S1/SvImJ, C3H/HeJ, and BALB/CByJ. The WGS reads were placed uniquely on the MGSCv3 C57BL/6J assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 TCAACTCTCAGCCCCACTTAGCTCTGAGTCAGGCCTGGAACAAACGGCCACAGGAATGAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAAGCTGCCATAGCTGCTTGTCACTTCAAGAGGTCAAAGAAAATAGTGTTAACCATGAA 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 AAAAGCTGCCATAGCTGCTTGTCACTTCAAGAGGTCAAAGAAATAGTGTTAACCATGAA 360
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        genome
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                                                                                    Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
structure of variation in the laboratory mouse (6915), 574-578 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C2ECHII/E1"
/db_xref="taxon:10090"
/map="- 19 22-610 35751955-35751368"
/clone_lib="CZECHII/E1"
                                                                                                                                      Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155
                                                                                                                                                                    Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: None
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Best Local Similarity 98.6%;
Matches 656; Conservative
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320 Charles Street,
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                                                                                                                                                                     GCATTACTGAATGCTTTCAATGTCTTATAATGATGGTAGGTGGCATGTCATGGGCCTA
                                                                                                                                                                                                      ACTAAGTCTGGAATGAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGGCAGGGGTG
                                                                                                                                                      GCATTACTGAATGCTTTCAATTTCTCCTAATGCTGGTACGATGGCATGTCACAGGGCCAT
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                                                                  1540 TCTCTCTGTGCATCACTTCGGCCCGTTTTGGGGT--AGATCCTCTGATTAGCCTTCAGAT
                            Gaps
                          22;
  Length 2074;
                          Indels
Score 367.8; DB 9;
Pred. No. 5.9e-96;
0; Mismatches 162;
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ALS90622
ALS90622.
HTG; CARP; ribonuclease P.
Homo sapiens (human)
 15.6%;
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                          Conservative
            Local Similarity
1es 597; Conserv
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                            1699 AGGGCAGTGATGTGGTGCCAATGTCCAACAGACAGCTGTCCCCTGAC-TCTTGACAATAGG 1757
                                                                          1998 GTGTGGAGGGCCCAGCAGCCAACTCCAGGGATTCCTTC-CACGACAGAAAAACATAC 2056
                                                                                                                                                                                                                                2 (bases 1 to 2074)
Ainara, Y.
Direct Submission
Submitted (26-PEB-1999) Second Department of Internal Medicine,
Gunma University School of Medicine, 3-39-15 Showa-machi, Maebashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2074)
Aihara, Y., Kurabayashi, M., Tanaka, T., Sekiguchi, K., Tomaru, K., Kanai, H., Takeda, S. and Nagai, R.
Human CVARP 5'-flanking region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product="cardiovascular-specific cardiac ankyrin repeat
                                                                                                             CCTGATTCGCATACGCCGCGG-----CCAGCTTGTCATCTCCCTCTTGGGCTTCCCAGAC
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                                                             ATGACTCGCATTGCTGAGCGGTGTGGTCACTGCCAAAGGAATGACCCTCTCACATTTCTT
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/gene="CVARP"
1833. .>2074
/gene="CVARP"
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/gene="CVARP"
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/translation="MAVFADLDLRAGSDLKALRGLVETAAHLGYSVVAINHIVDFKEK
KQEIEKPVAVSELFTTLFIVQGKSRPIKILTRLTIIVSDPSHCNVLRATSSRARLYDV
VAVFPKTEKLFHIACTHLDVDLVCITVTEKLPFYFKRPPINVAIDRGLAFELVYSPAI
                                                                                                                                                                                                                 KDSTMRRYTISSALNLMQICKGKNVIISSAAERPLEIRGPYDVANLGLLFGLSESDAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MIR repeat: matches 13. .262 of consensus"
complement(4176. .4649)
/note="match: GSS: Em:AQ626500"
join(<4648. .4764,7467. .7538,14216. .14305,23179. .23887,
24284. .24321,44717. .24796,28974. .29381)
                         evidence=not experimental
product==hb320F15.1.1 (ribonuclease P (30kD) (RPP30))"
protein_id="CAC70100.1"
db_xref="GI:15717970"
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hote="L2 repeat: matches 1200. .1808 of consensus" 6884. .7196
/hote="AluJb repeat: matches 1. .312 of consensus"
                                                                                                                                                                                                                                          AAVSTNCRAALLHGETRKTAFGIISTVKKPRPSEGDEDCLPASKKAKCEG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2732 of consensus"
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'note="AluSx repeat: matches 1. .289 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat: matches 16. .112 of consensus"
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/note="HY1 repeat: matches 1. .42 of consensus"
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note="match: ESTs: Em:AW939965"
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16979. .17036
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2939. .3167
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257. .5439
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1907. .2434
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10798. .11076
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1086, 11219
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'note="MIR repeat: matches 30.
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1926. .2208
Gqene="bA320F15.1"
fnote="match: GSS: Em:B92129"
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5440. .5721
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gene="bA320F15.1"
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/gene="bA320F15.1"
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/note="HY1 :
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join(391. .472,3273. .3328,3962. .4018,4428. .4502,7467. .7538,
14216. .14305,23179. .23295,23858. .23887,24284. .24321,
24717. .24796,28974. .29083)
                                                                                                                        Submitted (19-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, Cabonic State of the Cabonic Sequence version replaced gi:14161205.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone: or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP: MORMPEP; Information on the WORMPEP database can be found in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          jóin(120. .472,3273. .3328,3962. .4018,4428. .4502,7467. .7538,
14216. .14305,23179. .23295,23858. .23887,24284. .24321,
42417. .24706,28974. .29381)
/gene="ba320F15.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ca.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10
RP11-320F15 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-320F15 It may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true left end of clone RP11-2361B8 is at 50012 in this sequence. The true right end of clone RP11-103A2 is at 100 in this
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI-11.2"
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/note="match: GSS: Em:AQ670367"
complement(1. .97)
/note="match: GSS: Em:AQ544636"
complement(1. .77)
/note="match: STS: Em:G56439
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/db_xref="taxon:9606"
/chromosome="10"
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'gene="bA320F15.1"
                                                  (bases 1 to 50111)
                                                                              Tracey, A.
Direct Submission
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19513 GACCGGTGTGGAGGGCCCAGCAGGGCCAACTCCAGGGATTCCTTC-CACGACAGAAAAA 49455
                                                                                                 49633 CAGACACTGAGTCTGGAATGAAAATTCACCTGCCTCTGAGTTGGCTCCTAATGGGGGTGG 49574
                                                                                                                                                                                                                                                             49573 GAGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCT 49514
                                                                                                                                                                                                                           GGGTGTGGCTTCCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATAA-CG 2244
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                                                                                                                                                 CAGACACTAAGTCTGGAATGAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGCAG
                                                                            TICTICCTGATICGCATACGCCGCGG-----CCAGCTIGTCATCTCCCTCTTGGGCTTCC
                                                                                                                                                                                                                                                                                                GCTGGTGTGGAGGGCTCCACAGGGCCAGTTCCAGGGGTTCATCCACAAGAGAGAAAAA
     GTGGGATGACTCGCATTGCTGAGCGGTGTGGTCACTGCCAAAGGAATGACCCTCTCACAT
                          49753 ATAGGATGACTTGCATTGCTGAGCGATGTGATCACCACCAAAGGAATGGCCCTCTCACAT
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Novel target genes for diseases of the heart
Patent: WO 0192567-A 19 06-DEC-2001;
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Sequence 19 from Patent WO0192567.
AX322775
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/db_xref="taxon:32644"
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BD09FINITION Shear stress-responsive DNAs.
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Best Local Similarity 82.6
Matches 171; Conservative
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                                                                                                                                                                                                                                        /note="match: GSS: Em:AQ876596"
join(23179: .22295,23858. .23887,24284. .24321,24717. .24796,
28974. .29072,30647. .30748,31596. .31680,33706. .34469)
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                                                                                                                                                                                                                                                                                                                                                                                                         /gene="bA320Fis.1"
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/note="match: STS: Em:G24365"
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                                                                                                                                                                                                                                                                                                                 /product="bA320F15.1.3 (putative isoform 3)"
/note="match: EST9: Em:BE567341 Em:AI292002 Em:BF684192
Em:BF435407 Em:AI740881 Em:AA651912 Em:BF438915"
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .6302 of consensus"
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19198. .19363
/note="LIME repeat: matches 5272. .5435 of consensus"
19489. .1992 Beat: matches 5. .478 of consensus"
/note="MLTIC repeat: matches 5. .478 of consensus"
21838. .22258
/note="LZ repeat: matches 2109. .2669 of consensus"
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/note="L2 repeat: matches 2636. .2710 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .133 of consensus"
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Pred. No. 7e-90;
0; Mismatches 129; Indels 16;
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24561. 24956
Gene="bA320F15.1"
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2531. 25458
'note="FLAM C repeat: matches 1. .1
complement(25417, .25863)
/note="match: GSS: Em:AQ712354"
26204. 26603
/note="mLAM2 repeat: matches 5888.
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17236. .17755
//gene="bA20F15.1"
/note="match: GSS: Em:AQ551877"
17709. .17972
                                                                                                                                                                                                    22440. .22946
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/gene="bA320F15.1"
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Best Local Similarity 78.2%;
Matches 521; Conservative (
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ORGANISM

ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS

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/produčt="nuclear protein"
/protein id="CAA58676.1"
/db_xref="G1:793841"
/db_xref="SPTREMBL:015327"
/translation="MMVLKVBELVTGKKNGNGEAGEFLPEDFRDGEYEAAVTLEKQED
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VEVVVKEBEBEL ITEPVDVPFLKAALENKLPVVBKFLSDKNNPDVCDEYRALHRA
CLEGHLAI VEKLMEGGOLI PFDMLESTAIHWASRGGNLDVLKLLLNKGAKISARDKL
LSTALHVAVRTGHYGCAEHLI ACEADLINAKOREGDTPLHDAVRLNRYKMIRLINYGA
DLNI KNCAGKTPMDLVLHWQNGTKAI FDSLRENSYKTSRIATF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 ccesciccascitárarascitas cescicares de conseneras de consecuencia de conse
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                 Submitted (05-JAN-1995) W. Chu, Hoffmann-La Roche, 340 Kingsland Street, Dept. of Inflammation/Autoimmune Disease, Hoffmann-La Roche, Nutley, NJ 07110, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 TCCCCTCCCTCTTCAGCTTCCCAGACACTGATTCTGGAATGAAATTCACCTGCCTCTGA
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STS; STS sequence; primer; sequence tagged site. Homo sapiens (human)
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/note="cytokine-inducible expression"
nuclear protein from human endothelial cells
J. Biol. Chem. 270 (17), 10236-10245 (1995)
95247734
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/note="nuclear localization signal"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152. .283
/note="ankyrin-like repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="endothelial"
/tissue_type="skin"
/clone_lib="HDWEC cDNA"
1. 1901
94. 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .1901
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2284 ITCAICCACAGAGAGAGAAAACAIAGA 2310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 TTCCTTC-CACGACAGAAAACATACA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460 g
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                                                                                                                                                                        (bases 1 to 1901)
                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                      7730328
                                                                                                                                                                                                                   Chu, W.
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                          MEDLINE
PUBMED
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TITLE
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                                                   JOURNAL
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ORIGIN
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12. (Daesa 1 to 1901)

13. (Daesa 1 to 1901)

14. Yoshisue, H., Yoshisue, H., Ota, T., Kawabata, A., Sakine, B., Nakamura, Y. and Sugan, S.

15. Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.

16. Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.

17. Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.

18. Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.

18. Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.

18. Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.

18. Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.

18. Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.

18. Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.

18. Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.

18. Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.

18. Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.

18. Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.

18. Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.

18. Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.

18. Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.

18. Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.

18. Sakurada, K., Kuga, T., Sekine, S., Nakamura, Nakamura, S.

18. Sakurada, K., Kuga, T., Sekine, S.

18. Sakurada, M., Sekine, T., Sekine, S.

18. Sakurada, M., Sekine, T., Sekine, S.

18. Sakurada, M., Sekine, T., Sekin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-07T-2000 WO 2000JP006840
01-0CT-1999 JP 99P 280976
HIROSHI NOJIMA, HAJIME YOSHISUE, MASAYA OBAYASHI, TOSHIO OTA, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 GTTGGCTCCTAATGGGGGTGGGGGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCAC 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAZUHIRO SAKURADA, TETSURO KUGA, SUSUMU SEKINE, YUSUKE NAKAMURA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ankyrin-like repeat; nuclear localisation signal; nuclear protein.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chu, W., Burns, D.K., Swerlick, R.A. and Presky, D.H. Identification and characterization of a novel cytokine-inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C12N15/12, C07K14/435, C07K16/18, C12P21/02, C12Q1/68, A61K38/00, A61K39/395,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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H.sapiens mRNA for cytokine inducible nuclear protein.
X83703
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9
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Pred. No. 6.9e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db.xref="taxon:9606"
a _778 c 460 g 471
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    BD094076
BD094076.1 GI:22639664
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                                                                                                                             Homo sapiens (human)
Homo sapiens
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                                                                                      WO 0125427-A/37
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Best Local Similarity
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source

FEATURES

BASE COUNT ORIGIN

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2164

98

7

Gaps

2224

LOCUS DEFINITION ACCESSION VERSION

RESULT 13 HSRNACINP

KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

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ACU74094 160350 bp DNA linear HTG 01-SEP-2000
Homo sapiens chromosome 10 clone RP11-236B18, WORKING DRAFT
SEQUENCE, 17 unordered pieces.
                                                                                                                                                                                                                                                               2 (bases 1 to 160350)
Waterston, R.H.
Direct Submission
Submitted (13-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 160350)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                     MO 63108, USA
On Sep 1, 2000 this sequence version replaced gi:9665205
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2426: gap of unknown length 7519: contig of 5093 bp in length 7619: gap of unknown length 15286: contig of 7667 bp in length 15386: gap of unknown length 23150: gap of unknown length 23150: gap of unknown length 33663: contig of 10513 bp in length 50133: contig of 10510 bp in length 50133: contig of 10510 bp in length 50133: gap of unknown length 68088: contig of 17855 bp in length 68188: gap of unknown length 68188: gap of unknown length
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g of 1355 bp in length
f unknown length
g of 1655 bp in length
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unknown length
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                                                                                                                                                                                                                         The sequence of Homo sapiens clone Unpublished
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                                                                       AC074094
AC074094.3 GI:9958197
HTG: HTGS PHASE1: HTGS_DRAFT.
HOME SADIENS (human)
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113497: gap of v
141732: contig c
141832: gap of v
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143287: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2165 ATTGGCCACTGGTGGGGGCAGGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCAC 2224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prepared with primer pairs provided by Sandoz, derived from X83703
-- Washington University/Merck EST sequence.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2105 TCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATTCACCTGCCTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                    seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.5%; Score 128.6; DB 11; Length 1901; 82.6%; Pred. No. 6.9e-26;
                                                                                                                                                                                                                                                                                               Initial incubation: 94 degrees C for 90 seconds
                                                                                    Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Tel: 4157259687
Fax: 4157259689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                   94 degrees C for 15 s
62 degrees C for 23 s
72 degrees C for 30 s
30
                                                                                                                                                                                                                                                                                                                                                                                                      Perkin Elmer 9600
                                                                                                                                                                                                                                                                                                                                                                                                                                        25 ng
each 1 uM
each 200 uM
0.05 units/ul
10 ul
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/mol type="genomic DNA"
/db xref="taxon:9606"
/map="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCCTTC-CACGACAGAAAACATACA 232
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                                                                                                                                                                                                                                               CCAGATGGATGATCATGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 돌돌돌
                                                                                                                                                                                           Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                             Primer A. GGCATTTTGAAGGCATGG
Primer B. CCAGATGGATGATCATGA
STS size: 222
PCR Profile:
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50 r
20 8.3
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Annealing:
Polymerization:
PCR Cycles:
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Tag Polymerase:
Total Vol:
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                 1 (bases 1 to 1901)
Myers, R.M.
Unpublished (1996)
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1246. .1263
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Matches 171; Conservative
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primer_bind
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AUTHORS
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113587 GCATTACTGAATGCTTTCAATTTCTTATAATGGTAAGGTGGCATGTCATGGGGCCTA 113528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113647 TTAGAACACGGTAAGCATGTCATGTGCTAATTATGGCCAGTGACATAAAAGAAAAGT 113588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1658 GCATTACTGAATGCTTTCAATTTCTCCTAATGCTGGTACGATGGCATGTCACAGGGCCAT 1717
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52.5%; Pred. No. 2.9e-25;
tive 0; Mismatches 153; Indels 2;
1603 others
                                                                                                                                                                                                                                                 620. .15286
note="assembly_name:Contig12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8189. .88133
note="assembly_name:Contig17"
                                                                                                                                                                                                                                                                                                                                                                   note="assembly_name:Contig13"
                                                                                                                                                                                                                                                                                                                                                                                                    note="assembly_name:Contig14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="assembly_name:Contigl6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lote="assembly_name:Contig18"
.3498. .141732
                                                                                                                                                                                                                                                                                                                                                                                                                                     note="assembly_name:Contig15"
0234. .68088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="assembly_name:Contig19"
11833. .143187
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note="assembly_name:Contig5"
17387. .150852
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13288. .144942
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i0953. .153550
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57358. .160350
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53651. .157257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="assembly_name:Contig9"
32724 c 33135 g 45498 t
                                                                                                                                                                /organism="Homo sapiens'
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="10"
                                                                                                                                                                                                                                clone="RP11-236B18"
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Best Local Similarity 52.5'
Matches 171; Conservative
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Mouse high growth Mouse Presentiin-1 Phase-1 Rat CT gen Mouse high growth Wild-type mouse Wo Viral infection ge Mouse genomic regil Nucleotide sequenc ALPha 10cus of al Novel murine polyn Rat sequence diffe Mouse grastric antra Mouse grastric antra Mouse pre-AMP-18 g Murine LOBO genomi Murine LOBO senomi Hamster cholestero

Perfect score:

Sequence:

OM nucleic

о :

Run

Scoring table:

Searched:

Minimum DB seq Maximum DB seq

Database

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protein; CARP; cardiant; immunosuppressive; therapy; antisense gene therapy; mouse; ds.
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                                     ABT09109
ABX16390
ABA97708
                                                                                        ABN85733
ABL56461
ABL56463
                                                                                                                             ABS69028
ABK62570
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18105
659158
48974
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 WO200246220-A2
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89.2
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  Mouse CARP protein
Murine cardiac ank
Human CARP protein
Human polymucleoti
Human shear stress
Human CAAS6876 pro
Mouse gastric antr
Mouse gre-AMP-18 g
                                                                                  November 17, 2003, 23:28:30; Search.time 618.23 Seconds (without alignments) 10295.963 Million cell updates/sec
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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
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Result 8

Mouse retinoid met Mouse P450RAI geno Human SULF2 genomi Human DNA sequence Differentially exp Murine sequence fr Rat U3 gene trap d Partial mouse WRN Partial mouse WRN Mouse cell cycle r Rat U3 gene trap d Mouse alpha-1,3 ga Murine tumour necr Genomic DNA encodi Mouse poly Ig rece Mouse ES cell rela

The invention relates to a polynucleotide (I) comprising a fragment of a sequence upstream of the coding part of the gene for the Cardiac Ankyrin Repeat Protein (CARP). (I) is capable of inducing a specific expression in vivo of a gene operably linked to (I), in cardiac cells. (I) or a vector (IIb) comprising (I) is useful for the manufacture of a medicament in render for the treatment of cardiac insufficiency, cardiac hypertrophy and hypoxia, and for preventing rejection during cardiac transplant. An expression cassette under the control of (I) is useful for encoding a protein or RNA which is capable of activating the growth of cardiac cells, reducing or suppressing an immune response, inducing angiogenesis, correcting muscle contractility, cardiac hypertrophy, cardiac correcting muscle contractility. (IIb) is useful for expressing a gene of therapeutic interest in vivo, by isolating (IIb) and introducing (IIb) in the cardiac tissue, under conditions so that the gene of interest is expressed. (I), the vectors and the compositions are useful in clinical, expressed tissue, under conditions so that the gene of interest is caparimental, therapeutic and diagnostic fields, and in the treatment and prevention of cardiac pathologies. (I) is also useful for generating transgenic animals which constitute models for studying certain cardiac creaming molecules for their activity on the regulatory sequences of the gene encoding the CARP protein. The present sequence represents the DNA creament upstream of the coding sequence of a mouse CARP protein. sequence of a gene for Cardiac Ankyrin Repeat Protein, for controlling the level and specificity of expression of a transgene in cardiac muscle cells 1; Fig 1; 48pp; English Claim

Sequence 2358 BP; 636 A; 567 C; 542 G; 613 T; 0 other;

360 540 120 120 180 180 240 240 300 360 420 420 480 480 600 9 9 CATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTAT GATTGAAGGTCACCACAACATGAGGCCGCCACACTGTTCTAGAGAAAAATCACCTGGGTG GGCTTTGCCACCCATGAATACTTCCTAGTCTAGTCCGTTTGTGAAACTCAGCCCATCCA TTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGG GGGAATCAAACGACCCTTTACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTA CATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTAT GATTGAAGGTCACCACAAACATGAGGCCGCCACACACTGTTCTAGAGAAAAATCACCTGGGTG GGGAAAGGTTTGGGAAAGCCTTTCTGTCCATTCTTCATTCTTCAAAGTGATGTGTTCACA ACACTTCTGCAAGCCCCATCCTCTACAAGGTGCTCATTGGGAATTTCCTGGAGCTTCTCT 121 ACACTICIGCAAGCCCCAICCICTACAAGGIGCICCAIIGGGAAITICCIGGAGCTICICI GGGAAAGGTTTGGGAAAGCCTTTCTGTCCATTCTTCATTCTTCAAAGTGATGTTGTTCACA Gaps DB 24; Length 2358; ; 0 Indels ; 0 Query Match
100.0%; Score 2358;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2358; Conservative 0; Mismatches 181 61 61 181 241 301 361 541 121 241 301 361 421 421 481 g g ò g ò 유 ò g ઠે 8 8 g ò 엄 ð. g

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                                                                          TTATCCCCAGAAATAGGATGTCCCAAAGCAACACTTCCCAGCCAACTGGAGTGCTGATAA
                                                                                                              ACGTTAGTCATATGAGAGCTGACAAAGAAGGAAAAAAGAGCAGCGATGTGGTGCAATATTA
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                                                                                                                                                                                                                                                                        The invention relates to a human type-5 recombinant adenovirus vector for achieving cardiac-restricted transcription of a gene of interest. The vector comprises inverted terminal repeat (ITR) sequences from human adeno-associated virus (AAV) type 2 (AAAI0404) and a cardiac tissue-specific promoter. In particular, the promoter is that of the cardiomycoyte-restricted cardiac ankyrin repeat protein (CARP) gene. The adenovirus vector is used for targetted gene therapy for heart disease and for evaluating gene function. Cardiac restricted transcription of a transgene in both neonatal and mature cardiac tissues can be acchieved to treat inherited and acquired heart diseases. The vector is suitable for tissue-specific use in vivo and in vitro and provides cardiac restricted transcription. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     represents the murine cardiac ankyrin repeat protein (CARP) promoter
                                                                                                                                    Human type-5 recombinant adenovirus vector used for targeted gene therapy for heart disease and evaluating gene function contains a tissue-restricted promoter and inverted terminal repeat sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

74.8%; Score 1763.4; DB 21; Length 2247;
Best Local Similarity 91.2%; Pred. No. 0;
Matches 2124; Conservative 0; Mismatches 69; Indels 137; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2247 BP; 609 A; 549 C; 485 G; 589 T; 15 other;
                                                                                                                                                                                                                               Claim 8; Page 29-30; 33pp; English
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The invention relates to a polynucleotide (I) comprising a fragment of a sequence upstream of the coding part of the gene for the Cardiac Ankyrin Repeat Protein (CARP). (I) is capable of inducing a specific expression in vivo of a gene operably linked to (I), in cardiac cells. (I) or a vector (IIb) comprising (I) is useful for the manufacture of a medicament of intended for the treatment of cardiac insufficiancy, cardiac hypertrophy and hypoxia, and for preventing rejection during cardiac transplant. An expression cassette under the control of (I) is useful for encoding a protein or RNA which is capable of activating the growth of cardiac cells, reducing or suppressing an immune response, inducing angiogenesis, correcting muscle contractility, cardiac hypertrophy, cardiac collability and mycoraddisis. (IIb) is useful for expressing a gene of the cardiac tissue, under conditions so that the gene of interest is the cardiac tissue, under conditions so that the gene of interest is carperseated. (I), the vectors and the compositions are useful in clinical, experimental, therapeutic and diagnostic fields, and in the treatment and prevention of cardiac pathologies. (I) is also useful for generating cranspension annials which constitute models for studying certain cardiac pathologies. The transgenic animals are also useful for geneening concenting the CARP protein. The present sequences of the gene concent under content cardiac represents the DNA present sequences.
                                              New promoter sequence derived from a portion upstream of the coding sequence of a gene for Cardiac Ankyrin Repeat Protein, for controlling the level and specificity of expression of a transgene in cardiac muscle cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragment upstream of the coding sequence of a human CARP protein.
                                                                                                                                                                                                    Claim 5; Fig 2; 48pp; English
WPI; 2002-740642/80
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Sequence 2074 BP; 612 A; 469 C; 416 G; 572 T; 5 other;

2075 1657 1289 TCTATTICTIGACCACTCTGATCCATTTTGAAGTAAAATGCTCCAATTATTGCTGTT 1348 1405 GCATTACTGAATGCTTTCAATTTCTCCTAATGCTGGTACGATGGCATGTCACAGGGCCAT 1717 TTTAGCTGCAGACATCACTCCAGAGAATTCCAAACAGATAGAGACAAGTGGCACCCAGAC 1777 CCATCTCCCTTCCCCTCGGGCTGATTATCCCCCAGAAATAGGATGTCCCAAAGCAACACTTC 1837 CCAGCCAACTGGAGTGCTGATAAGTCCAGTTATCAGAAAGATATGGCTGTAAGTGTGATG 1897 1898 CACAGTGC--TTGCATTTTCTTGATACGTTAGTCATATGAGAGCTGACAAAGAAGGAAAA 1955 1642 TGTAGGGCATCTACATTTTCTTGATA-GGTAGTCATATGAAAGCTGACAAAGAA--AAAA 1698 1758 ATGACTTGCATTGCTGAGCGATGTGATCACCACCAAAGGAATGGCCCTCTCACATTTCTT 1817 1585 C---CTAAGTGAAGTGTTGATAAGTCTGCTTATCAGAAAGATATTACTGGGGGTGTGATA 1641 1525 ccagarccerrecerrasecretriracecassaarasearetecressacadaserrec 1699 AGGCCAGTGATGTGCCAATGTCAACAGACAGCTGTCCCCTGAC-TCTTGACAAATAGG 1540 TCTCTCTGTGCATCACTTCGGCCCGTTTTGGGGT--AGATCCTCTGATTAGCCTTCAGAT 1598 TTAGAACACGGTGAGCCTGTGGTGCACTAATTATGGCCAGTGACACCACTAGAGTCAAAGT ATGACTCGCATTGCTGAGCGGTGTGGTCACTGCCAAAGGAATGACCCTCTCACATTTCTT Gaps Score 367.8; DB 24; Length 2074; Pred. No. 5.9e-97; 0; Mismatches 162; Indels 22; 15.6%; 76.4%; Best Local Similarity 76.4 Matches 597; Conservative 1658 1406 1718 1466 1778 1838 2016 Query Match q g ò g ò 임 ò q ò g ઠે g ò g g δ ò ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, mematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaenia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
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                                                                                             TGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATATAA-CGGGCTG
                                                                                                                                                                1938 TTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCG
                                                                                                                                                                                                 GTGTGGAGGGGCTCCACAGGGCCAGTTCCAGGGGTTCATCACAAGAGAGAAAAACATAG
                                                               ACTAAGTCTGGAATGAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGCAGGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 13568; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polynucleotide SEQ ID NO 13568.
                                                                                                                                                                                                                                                                                                                                                                                 AAI93508 standard; cDNA; 1988 BP.
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18-MAY-2000; 2000US-0577409.
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P-PSDB; AAO13577.
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Human; congestive heart failure; dilative cardiomyopathy; sudden death; hypertroppic cardiomyopathy; ischaemic cardiomyopathy; rhythm disorder; heart muscle disease; conduction disorder; coronary heart disease; systemic arterial hypertension; pulmonary hypertension; endocarditis; pulmonary heart disease; valvular heart disease; pericardial disease; congenital heart disease; gene therapy; syncope; transgenic animal; expressed sequence tag; EST; clone X83703; CAA58676 protein; ds.
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                                                                                                         2165 ATTGGCCACTGGTGGGGGCAGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCAC
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'note= "AU-rich mRNA decay element"
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'note= "AU-rich mRNA decay element"
Pred. No. 1e-26;
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                        0; Mismatches
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/*tag= b
/note= "66268 cDNA fragment"
1604..1753
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/note= "SIMC01-1
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/note= "AU-rich
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            82.6%;
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/product=
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           Best Local Similarity 82.6
Matches 171; Conservative
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          but was obtained in electronic format directly from WIPO
                                                                                                                                                                                        2165 ATTGGCCACTGGTGGGGGCAGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCAC
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                                                                             DB 22; Length 1988;
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                                                                           Score 130.2; DB 22; Length
Pred. No. 3.6e-27;
0; Mismatches 33; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human shear stress-response coding sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stress-response protein; vascular disease,
                                                  Sequence 1988 BP; 632 A; 384 C; 472 G; 500 T; 0 other;
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Sugano S;
                      at ftp.wipo.int/pub/published_pct_sequences.
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Nakamura Y,
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                                                                           Query Match
Best Local Similarity 83.1%;
Matches 172; Conservative
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, Sekine S,
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P-PSDB; AAB90787.
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        specification,
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Kuga T,
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               957..3531
  number=
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 tissues and their corresponding proteins. The invention also relates to methode for assessing the expression level of these genes. The method is used for testing the predisposition of mammals and preferably humans for a heart disease or for an acute state of such a disease. It is also useful to treat disease of the heart such as congestive heart failure, dilative cardiomyopathy, hypertrophic cardiomyopathy, ischaemic cardiomyopathy, ischaemic cardiomyopathy, specific heart muscle disease, rhythm and conduction disorders, syncope and sudden death, coronary heart disease, valvular heart disease, congential heart disease, pericardial disease and endocarditis. Sequences of the invention are also used in gene therapy. A transgenic non-human mammal comprising the sequences of the invention are useful for the development for medicaments for the treatments of heart diseases. The present DNA sequence is expressed sequence tag (EST) clone X83703 which encodes CAAS8676 protein.
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                     Identifying a subject at risk for a heart disease e.g. congestive heart failure, dilative cardiomyopathy, heart muscle disease, by quantifying the polypeptide expressed by genes abnormally expressed in heart tissue
                                                                                                                                                                                                                                                                                                                                                                                         27 TCCCCTCCCTCTTCAGCTTCCCAGACACTGATTCTGGAATGAAAATTCACCTGCCTCTGA
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                                                                                                     The patent discloses novel target genes abnormally expressed in heart
                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                         Score 128.6; DB 24; Length 1901;
Pred. No. 1e-26;
0; Mismatches 34; Indels 2;
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/product= "Mouse pre-AMP-18"

/note= "contains introns"
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                                                                              Claim 2a; Fig 10b; 154pp; English.
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                                                                                                                                                                                                                                                                                                                            5.5%;
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Matches 171; Conservative
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P-PSDB; AAE16633.
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growth
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The present sequence is that of a gene encoding a novel member of the murine gastrokine group, designated antrum mucosal protein 18 (AMP-18). AMP-18 was initially detected in mammalian gastric antrum mucosa by a differentially detected in mammalian gastric antrum mucosa by a differential screen of CDNA libraries obtained from a mouse library (see ABZ24608). Genomic AMP-18 DNA sequences were subsequently cloned as a prelude to the analysis of gene regulacory elements. AMP-18 protein is expressed at high sequences mucosal cells. Partially purified AMP-18s from mouse and pig antrum tissue are mitogenic to confluent stomach mouse and pig antrum tissue are mitogenic to confluent stomach and kidney epithelial cells in culture. This effect is inhibited and kidney epithelial cells in culture. This effect is inhibited and kidney epithelium following damage by agents such as alcohol, the stomach epithelium following damage by agents such as alcohol, con-steroidal antiinflammatory drugs, or pathogens, particularly Helicobacter pylori, a causative agent of gastric ulcers and possibly cancers. AMP-18 protein, or an active peptide of AMP-18, is used in a claimed method of stimulating the growth of epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gastric Antrum Mucosal Protein 18, useful for preparing a composition for healing of the injured gastrointestinal tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agarwal K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Powell CT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 4; 67pp; English.
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6636..6641
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Walsh-Reitz M;

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Protein inhibitor, useful for treating gastrointestinal disorders or diseases comprises isolated homologous cellular stimulating proteins
                                          29-MAR-2002; 2002WO-US09885.
                                                          29-MAR-2001; 2001US-0821726
                                                                                       Martin TE,
                                                                        (UYCH-) UNIV CHICAGO
                                                                                                      WPI; 2003-103239/09
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              WO200278640-A2.
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                                                                                       Poback GF,
                                                                                                                                                                                                                                                                                                                                                                                                        ABZ82337
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                                                                                             TT-ACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTACATTACGATTCGTAAC 316
                                                               198 TCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGGAATCAAACGACCCT
                                                  Gaps
                                                                                                                                                                                                                                        protein; gastric antrum mucosal protein; gastro-intestinal disorder; cell therapy,
                                                  'n
                                                                                                                          AGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTG 365
                                                                                                                                         557
                                   4.0%; Score 95; DB 25; Length 7280;
80.5%; Pred. No. 1.6e-16;
Live 0; Mismatches 30; Indels
                                                                                                                                        AGTAGCAAAATT - - AGTTAGGAAGTAGGAACAAATAACGTTATGGTTG
                    Sequence 7280 BP; 2131 A; 1597 C; 1606 G; 1944 T; 2 other;
     cells in the gastrointestinal tract.
                                                                                                                                                                                                                                                                            ocation/Qualifiers
906..1956
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/number= 2
3673..3813
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4706..5607
/*tag= h
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/*tag= k
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/*tag= b
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Matches 136; Conservative
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                                                          The invention relates to a protein inhibitor which comprises homologous cellular growth stimulating proteins designated gastrokines. The invention also provides gastric antrum mucosal proteins designated AMP-18 which belongs to the novel group of gastrokines and nucleic acid molecules encoding such proteins. Pharmaceutical composition comprising growth stimulating peptide derived from a gastrokine protein is useful for treating gastro-intestinal disorder or diseases associated with overgrowth of gastric-intestinal disorder. The invention is useful in cell therapy. The present sequence is mouse pre-AMP-18 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451 TTCACAGGGTCACATATCAGATATCCTGCATCTTAGCTATTTACATTATGATTCATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 TCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGAATCAAACGACCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              composition; food intake disorder; body weight disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 7280;
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7280 BP; 2131 A; 1597 C; 1606 G; 1944 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.0%; Score 95; DB 25;
80.5%; Pred. No. 1.6e-16;
trive 0; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 histamine receptor H3; anorectic; gene; ds.
Disclosure, Fig 4; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ82337 standard; DNA; 18105 BP
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208828 GCAGCAGTTCCCAACGTGTGGGTCCAGATCTCTTTGGGAG-CCGAAAGGGCCTTTCACAG 208886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 AAATTACAGGTATGAAATAGCAATGAAATTATTA----TGATTGAAGGTCACACAAC 379
                                                                                                                                                                                                                         Sequence 659158 BP; 177521 A; 147222 C; 149414 G; 184754 T; 247 other;
                                                                                                                                                                                                                                                                                                                        204 GCAGCAGTICTCAACCTGGGGGCCTCGACCCCTTTGGGGGAATCAAACGACCCTTTACAG
                                                                                                                                                                                                                                                                                                                                                                                      264 GGGTCACATATCATCTATCCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAGCA
The invention describes an isolated nucleic acid molecule encoding a
             gene product that, when knocked out, results in a high growth (hg) phenotype. For example a nucleic acid disrupting the Socs2 gene is unseful for producing an animal characterised by a hg phenotype, by inhibiting expression of Socs2 (supressor of cytokine siganling 2) gene. The nucleic acids of the invention are useful for regulating body size in mammals. gene. The nucleic acids of the invention are useful for regulating body size in mammals. This sequence represents the mouse high growth region.

Note: This sequence did not form part of the printed specification but was obtained in electronic format directly from the US patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuron-specific transcription; promoter; mouse; Presenilin-1 gene; transgenic; laboratory model; Alzheimer's disease; ss.
                                                                                                                                                                                                                                                        Length 659158;
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                     Query Match 3.8%; Score 88.8; DB 25; Best Local Similarity 74.7%; Pred. No. 1.3e-13; Matches 139; Conservative 0; Mismatches 42;
                                                                                                                                                                                           segdata.uspto.gov/seguence.html?DocID=20020155564
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                                                                                                                                                      The invention relates to novel drug compositions for the treatment and prevention of disorders of food intake and body weight containing as the active component histamine receptor H3 protein, or DNA encoding it, or an agonist to it. A composition of the invention has anorectic activity. Compositions containing the histamine receptor H3 protein may be used in the treatment and prevention of disorders of body weight and food intake. The present sequence represents the mouse histamine receptor
                                                                                                                                                                                                                                                                                                                                                                                                      310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370
                                                                                                                                                                                                                                                                                                                                                                                                                           10825 CAACCCCTTTGGGGGGTCACATATCAGATATCCTGCCTATCAGATGTTTATACTGTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTTACAGTAGCAAAATTACACTTATGAAGTAGCAACAAAATAATTTTATGGTTGGGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel gene that when downregulated or knocked-out, results in high growth phenotype, useful for regulating body size in mammals e.g. rodent, bovine and canine -
                                                                            Histamine receptor H3 protein and its agonists and antagonists for treatment and prevention of body weight and food intake disorders
                                                                                                                                                                                                                                                                                                                                     3.8%; Score 89.2; DB 25; Length 18105; 79.1%; Pred. No. 1.3e-14;
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                                                                                                                           Example 1; Page 53-65; 73pp; Japanese
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               Takahashi K,
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                                           WPI; 2003-221596/21
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15325 A-CCTTTTCACAAGGGTCACACATCAGAGATCCTGCATATCCGATATTTATGTTATGATT 15267
                                                                                                                                                                                                                               15385 GCTACACTCTAGATCGGTGGTTCTCAAGCTGGGGGTCGCGACCCCTTTGGGGGGTTGGACA 15326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method used for evaluating the toxicity of an agent comprising determining the expression of a rat toxic response gene(9) in the test animal in response to the agent. The method is useful in drug development, particularly for conducting toxicity studies and analysis before a new drug or compound is approved for human consumption or use. The method is also useful in determining toxicological responses to a new drug. This polynucleotide sequence represents a phase-1 rat CT gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  determining toxicological responses to a new drug, by determining the expression of rat toxicologically relevant genes in the test animal in
                                                                                                                                                                                            191 GCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCTTTGGGGGGAATCAAA
                                                                                                                                                                                                                                                                251 CGACCCTTTACAGGGGTCACATATCATCTATCTATATGTCAGGTATTTACATTACGATT
                                                                                                                                                                                                                                                                                                                                     CGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          toxicity study; rat toxic response gene; toxicological response; development; phase-1 rat CT gene; ds.
                                                                                                                                                           Gaps
   comprising the neuron-
mammals containing a DNA expression cassette comprising the neuron-
specific promoter are useful as laboratory models for studying the
function of the Presenilin gene, and for studying the etiology of
                                                                                      Sequence 48974 BP; 12579 A; 10749 C; 11189 G; 14438 T; 19 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Evaluating the toxicity of an agent, useful in drug development
                                                                                                                       Length 48974;
                                                                                                                                                           ä
                                                                                                                                                           Indels
                                                                                                                       Score 88.6; DB 20;
Pred. No. 3.5e-14;
O; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 155; 388pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phase-1 Rat CT gene SEQ ID No 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Farr SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                          15206 CACCATGACATGAAG 15192
                                                                                                                                                                                                                                                                                                                                                                                                         371 CACCACAACATGAGG 385
                                                                                                                       Query Match 3.8%;
Best Local Similarity 69.2%;
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABT09109 standard; DNA; 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2001; 2001US-264933P.
26-JUL-2001; 2001US-308161P.
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                                                   Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-674961/72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Farris G,
                                                                                                                                                                                                                                                                                                                                     311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat;
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                                                                                                                                                                                                 292 ACCCCTTTGGGGGTTAAATGACCCTTTCACATATCAAATATCAAATACCTGCAG 351
                                                                                                                                                                                                                                                             352 AGCAGATATTCACATTGCAATCCGCAACAGCAGCAAAATTACAGTTACGAAGTAGCAAAG 411
                                                                                                                                      232 GAGCCATCCCTCCAGCCCCAGCCTGTTTTTATGGAAGTGATTCTCAACTCATGGGTCATG
                                                                                                                                                                   231 ACCCCTTTGGGGG--AATCAAACGACCCTTTACAGGGGTCACATATCATCTATAT
                                                                                                                                                                                                                                 289 GTCAGGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATG
                                                                                                       GAGCTTCTCTTTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGGCCCTCG
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes an isolated nucleic acid molecule encoding gene product that, when knocked out, results in a high growth (hg) phenotype. For example a nucleic acid disrupting the Socs2 gene is useful for producing an animal characterised by a hg phenotype, by gene. The nucleic acids of the invention are useful for regulating body size in mammals. gene. The nucleic acids of the invention are useful for regulating body size in mammals. This sequence represents the mouse high growth region.

Note: This sequence did not form part of the printed specification but was obtained in electronic format directly from the US patent
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Э,
                                           707;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High growth region, high growth phenotype, Socs2, body size, supressor of cytokine signaling 2, ds, mouse.
                                        DB 24; Length
.9e-14;
es 69; Indels
                                                                         Indels
                                                                                                                                                                                                                                                                                             349 - AAATAATTTTATGATTGAAGGTCACCACAACATGAGGCC 387
                                                                                                                                                                                                                                                                                                                  Seguence 707 BP; 205 A; 174 C; 156 G; 169 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                segdata.uspto.gov/sequence.html?DocID=20020155564
                                                                         0; Mismatches
                                          Score 83.6;
Pred. No. 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 18; 49pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                     ABX16390 standard; DNA; 659158
                                        3.5%;
ilarity 67.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse high growth region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bradford E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA
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                                                     Best Local Similarity
Matches 148; Conserv
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                                                                                                       171
                                           Query Match
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useful for monitoring the efficacy of a drug against depression
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                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus sp.
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                                                                                                                                                                                                                       439300 GTAĞCAAAATCACAGTTATGAGGTAACAATGAAATGATTITIATGGTTG-GGGTCACCGCA 439242
                                                                                                                                                                439358 TT--CTGCGTAGCATATCAGACATCCTGCATATCAGATATTCCATTATGACACATAATG 439301
                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents the genomic DNA sequence of the wild-type mouse Wolfram Syndrome 1 (WFS1) gene used in the method of the invention. The specification describes a non-human transgenic mammal comprising a genome containing a single copy of a wild-type WFS1 gene and a modified WFS1 allele containing a must copy of a wild-type WFS1 gene and a modified wFS1 allele containing a must disrupts the function of wolframin, or its transgenic progeny. Wolframin is a predicted transmembrane protein expressed in many tissues including pancreas and brain. The transgenic nonhuman animals are useful as models for depression, particularly as models for depression in humans. The animals exhibit chronic stress-induced neurochemical and behavioural changes associated with depression. The transgenic animals are also useful for screening or identifying antidepressant agents, drugs or genes that may be employed to ameliorate or treat depression. The animals are also
                                                                                  198 TCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGAATCAAACGACCCT 257
                                                                                                                                        258 TTACAGGGGTCACATATCATCTATATGTCAGGTATTTACATTACGATTCGTAACA 317
                                                                                                                                                                                             318 GTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATGATGAAGGTCACCACA 377
Sequence 659158 BP; 177521 A; 147222 C; 149414 G; 184754 T; 247 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New transgenic non-human animals (mice), useful as models for depression, for monitoring the efficacy of a drug against depression, and for screening antidepressants, drugs or genes for ameliorating or treating depression -
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wolfram Syndrome 1; WFS1; transgenic; wolframin; brain; depression; stress-induced neurochemical change; behavioural change; mouse; drug screening; antidepressant; gene; ds.
                                                        3,
                            DB 25; Length 659158;
                                                        50; Indels
                          Score 82; DB 25;
Pred. No. 1.3e-11;
0; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Wild-type mouse Wolfram Syndrome 1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 19; Page 60-63; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                   ABA97708 standard; DNA; 10917 BP
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                        3.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                     Matches 135; Conservative
                                                                                                                                                                                                                                                                              439241 ACATGTGG 439234
                                                                                                                                                                                                                                                    378 ACATGAGG 385
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                                          Best Local Similarity
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10398 TTCACAGGGGTTGCTTGCCAAAGACCATCAGAAAACACAGGTATTTACATTCCAATTCAT 10457
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                                                                                                                                                                                                                                       197 TTCTAGGGCAGCAGCAGTTCTCAACCTGGGGGGCCTCGACCCCTTTGGGGGGAATCAAACGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 AACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATGATTGAAGGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                          TTTACAGGGGTCACATATCA---TCTATCCTATATGTCAGGTATTTACATTACGATTCGT
                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viral infection; tumour suppressor; cellular gene; rat; cancer; serum protein; inhibitor; malignant phenotype; HIV; influenza; hepatitis; retrovirus; immunodeficiency; ds.
                                                                           3.4%; Score 80.4; DB 24; Length 10917; 70.8%; Pred. No. 3.9e-12; ... indels 5;
Sequence 10917 BP; 2423 A; 2842 C; 2929 G; 2706 T; 17 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 82-83; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viral infection gene SEQ ID NO:75.
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                                                                       Query Match
Best Local Similarity 70.8°
Matches 136; Conservative
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177 CTCTTTCAGGATCAGCCTGATTCTAGGCCAGCAGTTCTCAACCTGGGGGCCTCGACCCCT 236
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                                                                                                                                                                                                                                                                                                                            237 TIGGG---GGAATCAAACGACCCT-TTACAGGGGTCACATATCATCTATCCTATATGTCA 292
                                                                                                                                                                                                                                                                                                                                                                                                                  293 GGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAAT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                           239 AATATTTACATTATGATTCATAGTAGTACTAGAATTACAGTTATGAAGTTACA---AAAT 295
anemia virus, caprine arthritis encephalitis virus or visna virus. Because the identified genes are non-essential to cell survival, the treatment methods can be used in subjects without serious detrimental effects to the subjects.
                                                                                                                                                                                                Gaps
                                                                                                                                                                                             7;
                                                                                                                                              Query Match 3.3%; Score 78; DB 18; Length 892; Best Local Similarity 70.5%; Pred. No. 5e-12; Matches 148; Conservative 0; Mismatches 55; Indels
                                                                                                          Sequence 892 BP; 224 A; 206 C; 185 G; 229 T; 48 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 AATTTTATAGCTGAGAGTCACCACAACATG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353 AATTITATGATTGAAGGTCACCACAACATG 382
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Sequence 183, App
Sequence 183, App
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Sequence 36, Appl
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Sequence 208, App
Sequence 207, App
Sequence 207, App
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Sequence 4, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 107, App
Sequence 107, App
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Sequence 3, Appli
Sequence 3, Appli
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Sequence 75, Appl
                                          November 17, 2003, 23:31:50 ; Search time 137.266 Seconds (without alignments) 7582.209 Million cell updates/sec
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                                                                                                                                                                                             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                     569978 segs, 220691566 residues
                                                                                                                                                                  Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                               nucleic search, using sw model
                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                               seq length: 0
seq length: 200000000
                                                                     US-10-005-337A-1
2358
                                                                                                                                                                                                                                                                                                Length DB
                                                                                                                                                                                                                                                                                                                                 37950
10614
10614
4164
4072
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29604
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6645
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26700
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                                                                      Title:
Perfect score:
                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                              38.8
38.6
38.6
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Maximum DB
                               OM nucleic
                                                                                     Sequence:
                                                                                                                     Searched:
                                                                                                                                                                                              Database
                                            Run on:
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22
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                       Sequence 3, Appli
Sequence 14, Appli
Sequence 3, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGT 370
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Sequence 1, A
Sequence 1, A
Seguence 3,
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Sequence
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Sequence
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Sequence
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Sequence 75, Application US/09171209

Sequence 75, Application US/09171209

GENERAL INFORMATION:

APPLICANT: VANDERBILT UNIVERSITY

305 Kirkland Hall

Nashville, TN 37240

TITLE OF INVENTION: MAMMALIAN GENES INVOLVED IN VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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69.2%; Pred. No. 3.9e-16;
iive 0; Mismatches 59;
                                                                                                                                             US-08-916-421B-1
US-08-462-509B-1
PCT-08-96-6-6-1
US-08-846-705-4
US-08-846-706-1
US-09-220-132-168
US-09-220-132-168
US-09-078-294-4
US-09-602-264A-1
US-08-602-264A-1
US-08-461-018A-1
US-09-61-018A-1
US-09-61-018A-1
US-09-622-540A-1
                          US-09-577-806-3
US-08-232-463-14
US-09-007-005-3
US-09-244-796-3
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Patent No. 6255473

GENERAL INFORMATION:
APPLICANT: Vitek, Michael P.
APPLICANT: Witsuda, No. 6255473iaki
APPLICANT: Witsuda, No. 6255473iaki
APPLICANT: Mitsuda, No. 6255473iaki
APPLICANT: Moses, Allen D.
TITE OF INVENTION: Presentiin-1 Gene Promote
FILE REFERENCE: VITEKPRESENILIN
CURRENT APPLICATION NUMBER: US/08/920,422A
CURRENT FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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Matches 135; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 TTGGG---GGAATCAAACGACCCT-TTACAGGGGTCACATATCATCTATGTCA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 TIGGGAGIGCGGICAAAIGACCCIAICACGGGGICICAAAIGAGAIATCCIGCAIAICA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 GGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAAT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 AATATTTACATTATGATTCATAGTAGTACCAGAATTACAGTTATGAAGTTACA---AAAT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 CTCTTTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
3.3%; Score 78; DB 4; Length 892;
Best Local Similarity 70.5%; Pred. No. 6.9e-14;
Matches 148; Conservative 0; Mismatches 55; Indels
                                                                                                                                                   COUNTRY: USA
ZIP: 30303-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                 ADDRESSEE: Needle & Rosenberg, P.C. STREET: 127 Peachtree Street, Suite 1200 CITY: Atlanta STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US97/06067
PTLING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Selby, Elizabeth
REGISTRATION NUMBER: 38,298
REPERENCE/DOCKET NUMBER: 22000.0061/P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404 688 9880
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 AATTTTATGATTGAAGGTCACCACAACATG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 AATTTTATAGCTGAGAGTCACCACACATG 325
                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/171,209
FILING DATE: 08-Mar-1999
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Ilya, Chumakov
TITLE OF INVENTION: PROSTATE CANCER GENE
FILE REFERENCE: GENSET. 18CPICP
CURRENT APPLICATION NUMBER: US/09/338, 907
CURRENT FILING DATE: 1999-06-23
EARLIER APPLICATION NUMBER: 08/996,306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-09-171-209-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 183, Application US/09338907
Patent No. 6265546
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 892 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
SEQUENCES:
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US-09-338-907-183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 TGAAATAGCAATGAAATATTTATGATGAAGGTCACCACAACATGAGG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.2%; Score 74.8; DB 3; 1
Best Local Similarity 80.0%; Pred. No. 6.5e-12;
Matches 88; Conservative 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INCORMATION:
APPLICANT: Cohen Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Ilya. Chumakov
APPLICANT: Ilya. Chumakov
APPLICANT: Bougueleret, Lydie
TILE REPERBNCE: GENSET, 018CP1
CURRENT APPLICATION NUMBER: US/09/218, 207
CURRENT FILING DATE: 1999-12-22
EARLIER FILING DATE: 1997-12-22
EARLIER FILING DATE: 1997-12-22
EARLIER FILING DATE: 1997-12-22
EARLIER FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 578
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER PILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 09/218,207
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SEQ ID NO 183
; SEQ ID NO 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 183, Application US/09218207
Patent No. 6346381
                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: exon
LOCATION: 5259..5328
OTHER INFORMATION: exon2
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
LOCATION: 12675..12791
OTHER INFORMATION: exon3
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: exon
LOCATION: 14621..14710
OTHER INFORMATION: exon4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
LOCATION: 21789..21950
OTHER INFORMATION: exon6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 23387. 23510
OTHER INFORMATION: exon7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: 25520..26016
; OTHER INFORMATION: exon8
US-09-338-907-183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: exon5
                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19822..19912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 1982;
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US-09-218-207-183
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REGISTRATION NUMBER: 31,298

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7215 GAATCTAAGTCAGTGCTTCTCAACCTGTGGATCACAACCCATGTAGGGGGTAGAGTCAAA 7156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7095 CATGACAGAAGCAAAATTATAGTTGTGAAGTAGCAATGAAAATAATTTCACAGTTGGGGG 7036
                                                                                                                                                                                                                                                                                                                                                                                                                                ---GAATCAAA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 CGACCCTTTACAGGGGTCACATATCATCTATATGTCAGGTATTTACATTACGATT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 CGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 35, Application US/08187453
Sequence 35, Application US/08187453
Patent No. 5753431
GENERAL INFORMATION:
APPLICANT: Chiang, John
TITLE OF INVENTION: Regulatory Elements and Transcription Factors
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE FOLSE FOLSE
ADDRESSEE FOLSE
ADDRESSEE FOLSE
ASSET 3000 K Street, N.W.; Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                     Length 10614;
                                                                                                                                                                                                                                                                                                                                                                                                                              195 GATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGG
                                                                                                                                                                                                                                                                                                                              Query Match 3.2%; Score 74.6; DB 1; L
Best Local Similarity 64.0%; Pred. No. 3.5e-12;
Matches 130; Conservative 0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187,453
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 13-0CT-1993
FILING DATE: 13-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/135,511
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLIANCE DATE: 3-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 18748/188
  18748/175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7035 TCACACATCAGGAAGGTAGA 7013
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 n ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 CACCACACATGAGGCCGCCACA 393
                                                      TELERY: 904136
INPORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 10614 base pairs
TYPE: nucleic acid
TYPE: nucleic scingle
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                       TOPOLOGY: linear . . MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-187-453-35/c
                                                                                                                                                                                                                                                                                      US-08-135-511-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 ATCTATCCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTA
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US-08-135-511-35/c
; Sequence 35, Application US/08135511
; Patent No. 5558999;
; Patent No. 5558999;
; TITLE OF INVENTION:
; TITLE OF INVENTION: Regulatory Elements and Methods for Using Them
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9630 CGCAATATCAACAAAATATTTATGGTTGAGGGTCACCATAACGTGAGG 9679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 TGAAATAGCAATGAAATAATTTTATGATTGAAGGTCACCACAACATGAGG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 37950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 74.8; DB 4; Length 379
Pred. No. 6.5e-12;
0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC COMPATIBLE
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIR Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/135,511
TITING DATE: 13-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.2%;
80.0%;
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NAME: SANDERCOCK, Colin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.09
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3000 K Street, CITY: Washington, D.C.
                                                                                                                                                                                                                                                                       NAME/KEY: exon
LOCATION: 14621..14710
OTHER INFORMATION: exon4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: exon
LOCATION: 25520..26016
OTHER INFORMATION: exon8
                                                                FEATURE:
NAME/KEY: exon
LOCATION: 5259..5328
OTHER INFORMATION: exon2
                                                                                                                                                                                 NAME/KEY: exon
LOCATION: 12675..12791
OTHER INFORMATION: exon3
                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 19822..19912
OTHER INFORMATION: exon5
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OTHER INFORMATION: exon6
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LOCATION: 23387..23510
OTHER INFORMATION: exon7
                 TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: exon
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Gaps

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1252 AGAGCTTTTCAACCTGTGGGTCGTGACCCCTTCACGGAGCCAAACAACCTTTCAGAAGG 1311
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                                                                                                                                                                                                        206 AGCAGITCICAACCIGGGGCCTCGACCCCTTTGGGGGAAICAAACGACCCTTTACAGGG 265
                                                                                                                                                                                                                                                                                               266 GTCACATATCATCTATCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAGCAAA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 GACCGTAGAGCACAGGTTCTCAATCTGTGGGTCGCAACCCCTTT-GGGCATCCAAAAGCA 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               // Sequence 7, Application US/09272496
// Patent No. 6245966
// GENERAL INFORMATION:
// APPLICANT: DeGregori, James
// TITLE OF INVENTION: Adenoviral mediated gene transfer into lymphocytes
// FILE REFERENCE: 90-98
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                                                                                                                                                         51; Indels
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Pred. No. 1.4e-10;
0; Mismatches 49;
                                                                                                         Query Match
3.1%; Score 73.4; DB 4;
Best Local Similarity 70.2%; Pred. No. 4.7e-12;
Matches 127; Conservative 0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/272,496
CURRENT FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: US 60/092782
EARLIER FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 TIGAAGGICACCACAACAIGAGG 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-08-781-891-208/c
; Sequence 208, Application US/08781891
; Patent No. 6090620
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.9%;
ilarity 69.5%;
Conservative (
TYPE: nucleic acid
STRANDEDNESS: singl
TOPOLOGY: linear
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CORGANISM: Mus musculus
US-09-272-496-7
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                                            ; TOPOLOGY:
US-08-882-164D-38
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Best Local Simi
Matches 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 CGACCCTTTACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTACATTACGATT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 CGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGAAGGT 370
                                                                                                                                                                                                                                                                                                                                                                                        195 GATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCTTTGGGG----GAATCAAA
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                          Query Match

3.2%; Score 74.6; DB 1; Length 10614;
Best Local Similarity 64.0%; Pred. No. 3.5e-12;
Matches 130; Conservative 0; Mismatches 69; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage COMPUTER: COMPAQ, IBM PC compatible OPERATING SYSTEM:
MS-DOS-5.1
SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/82,164D
FILING DATE: JUNE 25, 1997
FILING DATE: JUNE 21, 1996
FILING DATE: Occober 1, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: Occober 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: HUNC, JOHN C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKT NUMBER: 36,424
REJECTRATION NUMBER: 36,4344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-882-164D-38
; Sequence 38, Application US/08882164D
; Patent No. 6306624
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; VUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7035 TCACACACATCAGGAAGGTAGA 7013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 CACCACACATGAGGCCGCCACA 393
                TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INPORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 10614 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4164 base pairs
                                                                                                                                                                                                        linear
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COUNTRY: Canada
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                                                                                                                                                                                                     TOPOLOGY:
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STATE:
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5983 TTACATCACAATTCATAACGGTGGCAAAATTACAGTCAAGAAGTAGCAAAGGAAATAATG 5924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 TTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.9%; Score 68; DB 4; Length 16442;
66.2%; Pred. No. 5e-10;
tive 0; Mismatches 50; Indels
                                                                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Y., Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Juhko
APPLICANT: Schellenberg, Gerald D.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GRNE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
CORRESPONDENCES: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/618,166
FILING DATE: 17-Jul-2000
CLASSIFICATION: *UDKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: MCMGGECF, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.419C1
TELEPHONE: (206) 622-4900
TELEFAN: (206) 622-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5923 icarggirggréccarcacageacadad 5896
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CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUCHWARE,
SUCHERNT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
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Patent No. 6090620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 16442 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.24
Matches 98; Conservative
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CLASSIFICATION:
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US-08-781-891-207
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Yu, Chang-En
Oshima, Junko
Mulligan, John T.
Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.9%; Score 68; DB 3; Length 164
Best Local Similarity 66.2%; Pred. No. 5e-10;
Matches 98; Conservative 0; Mismatches 50; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Oshima, Junko
APPLICANT: Schellenberg, Gerald D.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
UNDER OF ROUTHOUS: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PROPER PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5923 rcargerregreccarcacacacaca 5896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION WINBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 208, Application US/09618166
Patent No. 6583112
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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18748 AGCGACCCTTTCACAGATATCCTGAATATCAGGTATTTACATCGTGATTCATAGCAGTAA 18807
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                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-380-403A-4/c
US-08-380-403A-4/c
Sequence 4, Application US/08380403A
Sequence 4, Application US/08380403A
Sequence 4, Application US/08380403A
Setent No. 5831024
GENERAL INFORMATION:
MAPPLICANT: MINATO, Magahiro
APPLICANT: HATTORI, Masakazu
APPLICANT: HATTORI, Maeda
TITLE OF INVENTION: SPA-1 PROTEIN AND GENE CODING THEREFOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
Score 65.6; DB 4; Length 29604;
Pred. No. 4e-09;
0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                       18808 CAAAATTACAGTTATGAAGTACCAATGAAATCATTTTATGGTTG 18851
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CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
TILING DATE:
TO SASSITEMEN:
TILING DATE:
TO SASSITEMEN:
TO SASSI
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3000 K Street, N.W., Suite 500
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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      2.8%;
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Query Match
Best Local Similarity 76.9%
Matches 80; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: double
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TTY: Washington
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LOCATION:
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Oshima, Junko
Mulligan, John T.
Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 65.6; DB 3; Length 29
Pred. No. 4e-09;
0; Mismatches 24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIE: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPBY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MCMASTERS, DAVID D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.419C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/618,166
FILING DATE: 17-041-2000
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                          NAME: No. 6090620tenburg Ph.D., Carol REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-691
INFORMATION FOR SEQ ID NO: 207: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 207:
US-09-618-166-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 207, Application US/09618166 Patent No. 6583112 GENERAL INFORMATION:
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 207:
SEQUENCE CHARACTERISTICS:
LENGTH: 29604 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.8%;
                                                                                                                                                                                                                                                                                            LENGTH: 29604 base pairs
TYPE: nucleic acid
TYRANDEDNESS: single
TOPOLOGY: linear
US-08-781-891-207
   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fu, Ying-Hui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 76.9
Matches 80; Conservative
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US-09-618-166-207
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291 CAGGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAA 350
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                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MINATO, Nagahiro
HATTORI, Masakazu
HIROSHI, Kubota
MASATSUGU, Maeda
TITLE OF INVENTION: SPA-1 PROTEIN AND GENE CODING THEREFOR
NUMBER OF SEQUENCES: 7
  ..4903, 5017..5117, 5200..5255, 5447..5525, 5598
                                                                                            Length 6645;
                                                                                          2.8%; Score 65; DB 2; Length 664
72.3%; Pred. No. 2.5e-09;
live 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,810D
FILING DATE: 17-Jul-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
REFRENCE/DOCKET NUMBER: 53466/128/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                351 ATAATTTTATGATTGAAGGTCACCACAACATGAGG 385
                                                                                                                                                                                                                                                                                                                                                                                         434 AATAATTTTGA-TCAGGGTCACCACACCATGTGG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 30-7AN-1995
APPLICATION NUMBER: US 08/325,909
FILING DATE: 19-0CT-1994
APPLICATION NUMBER: UP 6-279712
FILING DATE: 20-0CT-1994
APPLICATION NUMBER: UP 6-139513
FILING DATE: 30-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/380,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08895810D Patent No. 6406886
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6645 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                          Query Match
Best Local Similarity 72.33
Matches 112; Conservative
                           ..5741)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-895-810D-4/c
                         ; LOCATION:
US-08-895-628-4
      LOCATION:
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                                                                                              291 CAGGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAA 350
                                                                                                                                                                                                494 CAGGTGTTTATGGTACAATTCCTAAGGGTAGCAGAATTACAGTTATGAAGTGGCAATGAA 435
                                                                   233 CCCTTTGGGGGAATCAAACGACCCTTTACAGGGGTCACAT--ATCATCTATATGT
                           Gaps
                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(904..1015, 1356..1459, 1726..1883, 2009
..2618, 2890..3164, 4291..4509, 4598..4709, 4795
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08895628
Patent No. 5998585
GENERAL INFORMATION:
APPLICANT: MINATO, Nagahiro
APPLICANT: HIROSHI, Rubota
APPLICANT: HIROSHI, Rubota
APPLICANT: MASATSUGU, Maeda
TITLE OF INVENTION: SPA-1 PROTEIN AND GENE CODING THEREFOR NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
    Pred. No. 2.5e-09;
0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,628
                                                                                                                                                                                                                                                351 ATAATTTTATGATTGAAGGTCACCACAACATGAGG 385
                                                                                                                                                                                                                                                                                        434 AATAATTTTGA-TCAGGGTCACCACCATGTGG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/128/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNDERS: US 08/380,403
FILING DATE: 30-JAN-1995
PILING DATE: 19-COT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/325,909
FILING DATE: 20-COT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 6-139513
FILING DATE: 30-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAMME: WEGNER, HAROLIC C.
NAMME: WEGNER, HAROLIC C.
NAMME: WEGNER, HAROLIC C.
Best Local Similarity 72.3%;
Matches 112; Conservative
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DELCG...
TELEPHONE: (202) 0.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-08-895-628-4/c
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LOCATION:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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Search completed: November 18, 2003, 07:06:16 Job time : 147.266 secs

Sequence 158, App Sequence 42, App Sequence 62, Appl Sequence 62, Appl Sequence 75, Appl Sequence 75, Appl Sequence 55, Appl

Sequence 182, 7 Sequence 158, 7 Sequence 421, 7

Sequence 55, Appl Sequence 52, Appl Sequence 26, Appl Sequence 107, Appl Sequence 115, Appl Sequence 115, Appl Sequence 319, Appl Sequence 567, Appl Sequence 567, Appl Sequence 567, Appl Sequence 44, Appl Sequence 3, Appl

Sequence 29, Appl Sequence 67, Appl Sequence 6, Appli Sequence 10, Appli

nucleic

Run on:

Sequence:

Searched:

Database

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Sequence 1, Application US/10005337A

Sequence 1, Application US/2003003984A1

Sequence 1, Application No. US2003003984A1

GENERAL INFORMATION:
GENERAL SCHWARTZ, Bertrand

APPLICANT: BRANGILE, Bertrand

APPLICANT: BRANGILES. Didier

APPLICANT: BRANGILES. Didier

APPLICANT: Didier

APPLICANT: Didier

APPLICANT: CANTENON: THEM AND USES THEREOF

FILLE OF INVENTION: THEM AND USES THEREOF

FILLE OF INVENTION THEMBER: US 60/251,582

FRIOR APPLICATION NUMBER: US 60/251,582

FRIOR APPLICATION OWNER: 2000-12-07

NUMBER OF SEQ ID NOS: 5

SEQ ID NO 1

SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ACACITICIGCAAGCCCCAICCICIACAAGGGGCTCATIGGGAATTICCTGGAGCTTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACACTTCTGCAAGCCCCATCCTCTACAAGGTGCTCATTGGGAATTTCCTGGAGCTTCTCT
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12 US-10-265-071-24

10 US-09-974-298-182

12 US-10-240-965-158

12 US-10-240-965-158

14 US-10-175-523-97

14 US-10-175-523-75

14 US-10-044-187-21

14 US-10-044-187-21

15 US-09-924-25

16 US-09-924-25

17 US-10-125-994A-25

18 US-10-125-994A-26

19 US-09-128-446-115

10 US-09-128-446-115

10 US-09-128-446-115

10 US-09-128-446-115

10 US-09-128-6146-115

10 US-09-128-6146-115

11 US-09-128-6146-115

12 US-10-155-661-567

13 US-10-144-592-3

13 US-10-044-592-93

13 US-10-044-592-93

13 US-10-044-592-93

13 US-10-044-592-93

10 US-09-860-44-15
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US-10-208-304-6
US-10-003-806-10
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larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                      TYPE: DNA
CORGANISM: Mus musculus
US-10-005-337A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 2358; Conserv
       US-10-005-337A-1
                                                                                                                                                                                                    63.8
63.2
63.2
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63
60.6
       71.6
69.4
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69.8
68.8
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67.8
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                                                                                                                                                                          November 17, 2003, 23:33:10 ; Search time 1128.46 Seconds (without alignments) 6829.176 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Sequence 2
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
                            5.1.6
Compugen Ltd.
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US-10-005-337A-2

US-10-105-523-80

US-09-771-208-20

US-09-771-208-20

US-09-771-208-20

US-10-105-533-97

US-10-002-631C-156

US-10-105-533-1

US-10-105-533-1

US-10-105-543-1

US-09-917-800A-477

US-09-917-800A-477

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US-09-917-800A-477

US-09-917-800A-477

US-09-917-800A-183

US-09-917-800A-183

US-09-917-800A-183

US-09-917-800A-183

US-09-918-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2169961 segs, 1634102185 residues
                            GenCore version (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                        nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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2358
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                                                    Copyright
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Match
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us-10-005-337a-1.rnpb

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APPLICANT: BOCKANGE, DESCRIPTION
APPLICANT: BOCKANGE, DESCRIPTION
APPLICANT: Hook, Derek
APPLICANT: Hook, Derek
APPLICANT: Alinczak, Leszek
APPLICANT: Alinczak, Leszek
APPLICANT: Laeng, Pascal
APPLICANT: Rajan, Prithi
ITLE OF INVENTION: MULT: PARAMETER HIGH THROUGHDUT SCREENING ASSAYS (MPHTS)
FILE REPERENCE: 3235/10795-U33
CURRENT APPLICATION NUMBER: US(10/175,523
CURRENT APPLICATION NUMBER: US 60/299,151
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/325,150
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1938 TIACTICGGTICCCAGGITGAAGATTAICTCACCCGGCCCCAGCTATAIAAGCTGACCG 1997
                                                                                                                                                                                                                                                                                                                         GTGTGGAGGGCTCCACAGGCCCAGTTCCAGGGGTTCATCCACAAGAGAAAAAACATAG 2309
                                                                                                                                                                                                                                                                                                                                                                                  1998 GTGTGGAGGGCCCAGCAGCCAACTCCAGGGATTCCTTC-CACGACAGAAAAATAC 2056
                                                                                                                                            TGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATATAA-CGGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56512 TCTATAGCAGTGGTTCTCAACCAGTGGCTCATAACCCCTATGGTGG-CTGAATGACCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 TTACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTACATTACATTCGTAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGTCACCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 90650;
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Pred. No. 5.7e-18;
0; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 80, Application US/10175523
; Publication No. US20030096264A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 139; Conservative
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; ORGANISM: Mus musculus
US-10-175-523-80
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US-10-175-523-80
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APPLICANT: SCHWARTZ, Bertrand
APPLICANT: SCHWARTZ, Bertrand
APPLICANT: BRANELLEC, Didier
APPLICANT: CHIEN, Kenneth R.
TITLE OF INVENTION: SEQUENCES UPSTREAM OF THE CARP GENE, VECTORS CONTAINING
TITLE OF INVENTION: THEM AND USES THEREOF
FILE REFERENCE: 03806.0530-00000
CURRENT APPLICATION NUMBER: US/10/005, 337A
CURRENT FILING DATE: 2001-12-07
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15.6%; Score 367.8; DB 14; Length 2074;
Best Local Similarity 76.4%; Pred. No. 3.4e-101;
Matches 597; Conservative 0; Mismatches 162; Indels 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/251,582
PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 2
LENGTH: 2074
                                                                                                                                                                                                                                                                 Sequence 2, Application US/10005337A Publication No. US20030039984A1 GENERAL INFORMATION:
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US-10-005-337A-2
                                                                                                                                                                             RESULT 2
US-10-005-337A-2
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APPLICANT: Hook, Derek
APPLICANT: Klimczak, Leszek
APPLICANT: Klimczak, Leszek
APPLICANT: Laeng, Pascanl
APPLICANT: Palfreyman, Michael
APPLICANT: Rajan, Prithi
TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
FILE REFERENCE: 3235/10795-053
CURRENT APPLICATION NUMBER: US/10/175,523
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-- TGATTGAAGGTCACCACAAC 379
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68.8%; Pred. No. 6e-13;
tive 0; Mismatches 58;
  324 AAATTACAGGTATGAAATAGCAATGAAATAATTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/299,151
PRIOR APPLICATION NUMBER: US 60/317,828
PRIOR APPLICATION NUMBER: US 60/315,150
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR PAPLICATION NUMBER: US 60/33,047
PRIOR PLING DATE: 2001-11-14
PRIOR PLING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
SEQ: 10 NO 97
                                                                                                                                                                                                                                                                            Sequence 97, Application US/10175523 Publication No. US20030096264A1 GENERAL INFORMATION: APPLICANT: Brockman, Jeffrey
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Patent No. US20020155564A1
GENERAL INFORMATION.
APPLICANT: MEDRANO, JUAN
APPLICANT: BRADFORD, ERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Mus musculus domesticus
US-10-175-523-97
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                                                                                                   380 ATGAGG 385
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US-09-771-208-20/c
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                                                                                                                                           APPLICANT: BRADFORD, ERIC
APPLICANT: HORVAT, SIMON
TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
FILE REFERENCE: 407T-923710US
CURRENT APPLICATION NUMBER: US/09/771,208
CURRENT FILING DATE: 2001-01-26
PRIOR FILING DATE: 1997-12-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
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LOCATION: (1390986)...(391005)
OTHER INFORMATION: n is unidentified a, c, NAME/KEY: misc feature
LOCATION: (1346860)...(346823)
OTHER INFORMATION: n is unidentified a, c, NAME/KEY: misc feature
LOCATION: (131774)...(317193)
OTHER INFORMATION: n is unidentified a, c, NAME/KEY: misc feature
LOCATION: (280353)...(280373)
OTHER INFORMATION: n is unidentified a, c, NAME/KEY: misc feature
LOCATION: (210829)...(271848)
OTHER INFORMATION: n is unidentified a, c, NAME/KEY: misc feature
LOCATION: (211829)...(271848)
OTHER INFORMATION: n is unidentified a, c, NAME/KEY: misc feature
LOCATION: (181872)...(181891)
OTHER INFORMATION: n is unidentified a, c, NAME/KEY: misc feature
LOCATION: (181872)...(181891)
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LOCATION: (602466)..(602485)
OTHER INPORMATION: n is unidentified a, c,
NAME/KEY: misc_feature
LOCATION: (546598)..(547017)
OTHER INPORMATION: n is unidentified a, c,
NAME/KEY: misc_feature
LOCATION: (494715)..(494814)
OTHER INFORMATION: n is unidentified a, c,
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LOCATION: (132680)..(132700)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (170625)..(170645)
OTHER INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (123459)..(123478)
OTHER INFORMATION: n is unidentified a,
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// OTHER INFORMATION: n is a, c, g, or
US-09-771-208-20
                                            Sequence 20, Application US/09771208 Patent No. US20020155564A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Mus musculus
                                                                                              GENERAL INFORMATION:
APPLICANT: MEDRANO,
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251 CGACCCTTTACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTACATTACGATT 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 CGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGAAGGT 370
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                                                                                                                          Sequence 156, Application US/10002631C

Publication No. US20030157486A1

GENERAL INFORMATION:
APPLICANT: Graff, Jonathon M.
APPLICANT: Muenster, Matthew
TITLE OF INVENTION: MERTHODS TO 1DENTIFY SIGNAL SEQUENCES
FILE REFERENCE: A34943 090495.0743

CURRENT FILING DATE: 2001-10-31

PRIOR APPLICATION NUMBER: 60/300, 309

PRIOR FILING DATE: 2001-06-21

NUMBER OF SEQ ID NOS: 324

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 156

LENGTH: 889
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%; Pred. No. 1.7e-12;
0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | FEATURE:
| NAME/KEY: unsure
| LOCATION: (1)...(203)
| OTHER INFORMATION: n = A, C, G or T
| US-10-002-631C-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10195963
Publication No. US20030167488A1
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. LOCATION:
. OTHER INFORMATION: m=a or c;
US-10-195-963-1
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APPLICANT: Roberds, Steven L
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Best Local Similarity 74.8°
Matches 101; Conservative
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Best Local Similarity 70.83
Matches 136; Conservative
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                                                                                                      US-10-002-631C-156
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US-10-195-963-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 TTACAGGGGTCACATATCATCTATATGTCAGGTATTTACATTACGATTCGTAACA 317
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APPLICANT: HORVAT, SIMON
TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
FILE REFRENCE: 407T-923710US
CURRENT APPLICATION NUMBER: US 09/771,208
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 08/999,477
PRIOR PILING DATE: 1997-12-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PALENTIN VERSION 3.0
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LOCATION: (123459) ...(123478)
LOCATION: (123450) ... (123478)
NAME/KEY: misc feature
LOCATION: (602465) ... (602485)
OTHER INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /KEY: misc feature
IION: (546998)..(547017)
R INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (271829) .. (271848)
OTHER INFORMATION: n is unidentified a,
NAME/KEY: misc feature
LOCATION: (183872) .. (183891)
OTHER INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEY: misc feature
ION: (494715)..(494814)
INFORMATION: n is unidentified a,
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LOCATION: (280353)..(280373)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (170625)..(170645)
OTHER INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'KEY: misc_feature
11ON: (390986)..(391005)
'INFORMATION: n is unidentified a,
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TION: (346B60)..(346823)
R INFORMATION: n is unidentified a,
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LOCATION: (317174)..(317193)
JTHER INFORMATION: n is unidentified
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; OTHER INFORMATION: n is a, c, g, or
US-09-771-208-20
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LOCATION: (132680)..(132700)
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                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                 SEQ ID NO 20
LENGTH: 659158
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Sequence 75, Application US/10228794
Publication No. US20030027198A1
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APPLICANT: BLOWING. Derikey
APPLICANT: Klinczak, Leszek
APPLICANT: Klinczak, Leszek
APPLICANT: Leeng, Pascal
APPLICANT: Leeng, Pascal
APPLICANT: Rajan, Prithi
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APPLICANT: Rajan, Prithi
APPLICANT: 2001-06-18
ARIOR FILING DATE: 2001-06-18
ARIOR FILING DATE: 2001-09-07
ARIOR APPLICANTON NUMBER: US 60/333,047
ARIOR FILING DATE: 2001-11-14
APRICR FILING DATE: 2002-01-18
APRICR FILING DATE: 2002-01-18
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                                                                                                                                                                                                                                                                                                                                                                      10458 GACAGTAGTAAAATTACAGTTATGCAGTAGCAATGAAATAATTATTATGGTTGGGTGAC 10517
                                                                                                                                                                                                                                   10398 TTCACAGGGGTTGCTTGCCAAAGACCATCAGAAAACACAGGTATTTACATTCCAATTCAT 10457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55602 Gaddicacacatcacatatcciccatatcaaatatitacattataattcataacactage 55661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 GGGGTCACATATCATCTATCCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAGC 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 AAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGTCACCACAACATG 382
                                                                                                                                                                     TTTACAGGGGTCACATATCA---TCTATCCTATATGTCAGGTATTTACATTACGATTCGT
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                                     TTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCC
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Pred. No. 6.2e-11;
0; Mismatches 28
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l Similarity 77.2%;
95; Conservative
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10518 CACATCATGAAG 10529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Brockman, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                        374 CACAACATGAGG 385
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Best Local Similarity
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LENGTH: 185548
                                  197
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RESULT 10 US-10-228-794-75

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 GGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATTAGAAATGAAAT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 CTCTTTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCT
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                                                  305 Kirkland Hall
Nashville, TN 37240
TITLE OF INVENTION: MAMMALIAN GENES INVOLVED IN VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                     ADDRESSEE: Needle & Rosenberg, P.C. STREET: 127 Peachtree Street, Suite 1200 CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 78; DB 14;
Pred. No. 1.5e-12;
0; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Selby, Elizabeth
REGISTRATION NUMBER: 38,298
REFERENCE/DOCKET NUMBER: 22000.0061/P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/228,794
FILING DATE: 27-Aug-2002
CLASSIFICATION: UNKNOWN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/171,209
FILING DATE: 08-Mar-1999
APPLICATION NUMBER: PCT/US97/06067
FILING DATE: CURROWN-
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 AATTTTATGATTGAAGGTCACCACAACATG 382
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MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-10-228-794-75
GENERAL INFORMATION:
APPLICANT: VANDERBILT UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                          STATE: Georgia
COUNTRY: USA
ZIP: 30303-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/10026188 Publication No. US20020164645A1 GENERAL INFORMATION:
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STRANDEDNESS: double
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Best Local Similarity 70.5%;
Matches 148; Conservative
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                                                                                                                                                        NUMBER OF SEQUENCES:
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US-10-026-188-3/c
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259 ACGIAITAGCIAICCTGGAIGTCAGAIATTIACATIACAATGTAIAACAGCAGCAGAATT 318
201 GTTCTCAACCTGTGGGTTACAACCCCTTTGAGGG--TCAAACGACCCTTTCACAAGAGTT 258
                                                                                                      269 ACATATCATCTATCCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAGCAAAATT
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66.7%; Pred. No. 3.3e-11;
iive 0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 477, Application US/09917800A Patent No. US20020119462A1
                                                                                                                                                                                                                                    329 ACAGGTATGAAATAGCA 345
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Best Local Similarity 66.7'
Matches 124; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238539 --GGAAGTCATATGACCCTTTCAAAGGCTTGCCTAAGACCATC--AGAAAATAGATATT 238484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 TACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAAT-GAAATAATTT 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 CITICAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 91, Application US/09728445

Sequence 91, Application US/09728445

Patent No. US20020102543A1

GENERAL INFORMATION:

APPLICANT: Friedrich, Glenn

APPLICANT: Zambrowicz, Brian

APPLICANT: Sands, Arthur T

TITLE OF INVENTION: No. US20020102543A1e1 Mutated Mammalian Cells and

TITLE OF INVENTION: Animals

FILE REFERENCE: LEX-0102-USA

CURRENT APPLICATION NUMBER: US/09/728,445

CURRENT FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/168,358

PRIOR FILING DATE: 1999-12-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.3%; Score 76.8; DB 13; Length 249487; 70.2%; Pred. No. 2e-10; ive 0; Mismatches 57; Indels 5;
                       APPLICANT: Zhang, Yifeng
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
TITLE OF INVENTION: Ion Channel
FILE REFERENCE: 02307E-114910US
CURRENT APPLICATION NUMBER: US,10/026,188
CURRENT FILING DATE: 2000-12-21
FRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 249487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 75.8; DB 10; Length 335;
Pred. No. 3.6e-12;
0; Mismatches 22; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
COTHER INFORMATION: mouse genomic region containing ltrpc5 US-10-026-188-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 891
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 91
LENCTH: 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)....(335)
; OTHER INFORMATION: n = A,T,C or G
US-09-728-445-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 81.8%;
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 70.2
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-728-445-91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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1; 4978 ACTCTAAGCCTGTGGTTCTCAACCCATGAGTCATGACCCTTTGGGATTGTCCAATGACCC 4919 4918 TTTTATCACAGGGGTCGAATAGTAGGTATCCTGTAGATCAGATATATACATTGCAATTCA 4859 256 CTTT---ACAGGGGTCACATATCATCTATATGTCAGGTATTTACATTACGATTGG 312 313 TAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGTCA 196 ATTICTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGGAATCAAACGACC 3; Gaps ; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AB009636 US-09-917-800A-477 Length 5990; CCACAA 378 373

4798 CTACAA 4793

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GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANTON NUMBER: US/09/901, 484A
CURRENT APPLICATION NUMBER: US 08/996,306
PRIOR FILING DATE: 1997-12-22
PRIOR APPLICATION NUMBER: US 09/99,658
PRIOR FILING DATE: 1998-09
PRIOR FILING DATE: 1998-09
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-06-13
PRIOR FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 578
SOFTWARE: Patentin version 3.1
SEQ ID NO 183
LENGTH 37950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (6167..(616)
OTHER INFORMATION: n = a, c, g, or t.
NAME/KEY: misc_feature
LOCATION: (1552)
OTHER INFORMATION: n = a, c, g, or t.
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LOCATION: (2821)..(2824)
OTHER INPORMATION: n = a, c, g, or t.
NAME/KEY: misc_feature
LOCATION: (2826)..(2826)
OTHER INFORMATION: n = a, c, g, or t.
                                                 Sequence 183, Application US/09901484A Patent No. US20020119460A1
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LOCATION: (2831)..(2833)
OTHER INFORMATION: n = a, c, g, or
NAME/KEY: misc feature
LOCATION: (2835)..(2835)
OTHER INFORMATION: n = a, c, g, or
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (2809)..(2809)
OTHER INFORMATION: n = a, c, g,
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LOCATION: (6247).. (6247)
OTHER INFORMATION: n = a, c, g,
NAME/KEY: misc_feature
LOCATION: (8667).. (8667)
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NAME/KEY: misc_feature
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LOCATION: (5259)..(5328)
OTHER INFORMATION: exon 2
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LOCATION: (8671)..(8679)
OTHER INFORMATION: n = a,
NAME/KEY: misc_feature
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OTHER INFORMATION: n = a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Mus musculus
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RESULT 14
US-09-901-484A-183
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9570 ACCTATCCTGCTTATCAGATAGTTACATTATGAATTGTAACAGCAGCAAAATCACAGTTA 9629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 37950;
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Pred. No. 2.2e-10;
0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (17639)...(17639)
OTHER INFORMATION: n = a, c, g, or t.
NAME/KEY: misc feature
LOCATION: (17707)...(17707)
OTHER INFORMATION: n = a, c, g, or t.
NAME/KEY: misc feature
LOCATION: (17867)...(17867)
OTHER INFORMATION: n = a, c, g, or t.
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COTHER INFORMATION: exon 8
NAME/KEY: misc feature
LOCATION: (37931)..(37931)
COTHER INFORMATION: n = a, c, g, or t. US-09-901-484A-183
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Patent No. US20020165345A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Ilya, Chumakov
                                                                                                                                                                                                                                                                                                                                                                                                                       or
                                                                           LOCATION: (18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687)...(18687
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80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAME/KEY: misc feature
LOCATION: (17578). (17578)
OTHER INFORMATION: n = a, c,
NAME/KEY: misc feature
LOCATION: (17639). (17639)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (12298)..(12298)
OTHER INFORMATION: n = a, c,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.0
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (12675)..(12791)
OTHER INFORMATION: exon 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (14621)..(14710)
OTHER INFORMATION: exon 4
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NAME/KEY: misc feature
LOCATION: (23387)..(23510)
OTHER INFORMATION: n = a,
NAME/KEY: misc feature
LOCATION: (8687)..(8687)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-853-526-183
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9570 ACCIAICCIGCTIAICAGAIAGITACAITAIGAAITGIAACAGCAGCAAAAICACAGITA 9629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.2%; Score 74.8; DB 10; Length 37950; Best Local Similarity 80.0%; Pred. No. 2.2e-10; Matches 88; Conservative 0; Mismatches 22; Indels 0;
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: PROSTATE CANCER GENE
FILE REFERENCE: GENEST.18CP1CP
CURRENT APPLICATION NUMBER: US/09/853,526
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 09/338,907
PRIOR PILING DATE: 1999-06-23
PRIOR PILING DATE: 1999-06-23
PRIOR PILING DATE: 1999-06-23
PRIOR PILING DATE: 1999-06-99
PRIOR FILING DATE: 1988-09-09
PRIOR FILING DATE: 1988-09-09
PRIOR FILING DATE: 1988-12-22
NUMBER OF SEG ID NOS: 578
SEQ ID NO 183
LENGTH: 37950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: exon

LOCATION: 5259.5328

OTHER INFORMATION: exon2

LOCATION: 12675..12791

OTHER INFORMATION: exon3

NAME/KEY: exon

LOCATION: 14621..14710

OTHER INFORMATION: exon4

NAME/KEY: exon

LOCATION: 19822..19912

OTHER INFORMATION: exon5

NAME/KEY: exon7

LOCATION: 21789..21950

OTHER INFORMATION: exon6

NAME/KEY: exon7

LOCATION: 23387..23510

OTHER INFORMATION: exon6

NAME/KEY: exon7

LOCATION: 2387..23510

OTHER INFORMATION: exon7

NAME/KEY: exon7

LOCATION: 2387..23510

OTHER INFORMATION: exon7

NAME/KEY: exon7

LOCATION: 2387..23510
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Mus musculus FEATURE:
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9630 CGCAATATCAACAAAATAATTTTATGGTTGAGGGTCACCATAACGTGAGG 9679 336 TGAAATAGCAATGAAATAATTTTATGATTGAAGGTCACCACAACATGAGG 385 ð

Search completed: November 18, 2003, 07:42:01 Job time : 1143.46 secs

(OTASU) NNAJB 3ĐA9 SIHT

CH230-164 CH230-164 1M0418D12

Mus muscu Mus muscu 2M0198P19 K0996B07-CH230-340 1M0319013 CH230-282 RPCI-23-2 UI-R-BT1-CH230-315 1M0085D24 1M0149M20 2M0014H04

2M0160A02

BY549634

CH230-427

CH230-525

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Title: Perfect score:

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Scoring table:

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Database

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BF543101 UI-R-AGI-AW252440 UI-R-BJO-AW252440 UI-R-BJO-AI710529 UI-R-AGI-AU139209 BEG7514 UW52608 y AZ804735 ZM0065113 AQ480395 RPCI-23-4 AZ29439 RPCI-23-5 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470798 BB470778 BB470798 B
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RPCI-24-330A6.TJ RPCI-24 Mus musculus genomic clone RPCI-24-330A6,
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BZ128535 CH230-298
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BZ223957 CH230-446
AZ060257 RPCI-23-4
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Sases 1 to 600)
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M.,
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,
Mussell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished
Other_GSSs: RPCI-24-330A6.TV
BI293043 UI-R-DK0
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
                                                                                                                                                                            AZ734079
BAZ734079
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AZ295534 RPCI-23-1
BY091041 BY091041
BY079997 BY079997
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            GenCore version (c) 1993 - 2003
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Score

Result Š.

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/sex="remail."
/lab_host="DH10B"
/clone lib="RPCT-23"
/clone lib="RPCT-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
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                                                                                                                                                                                                                       Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

Clones are derived from the mouse BAC library and library availability, please contact Pierer de Jong

(pieter@dejong.med.buffalo.edu. Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 105 row: P column: 3

Seq primer: SP6

Class: BAC ends.
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 586)
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      RPCI-23-105P3.TJ RPCI-23 Mus musculus genomic clone RPCI-23-105P3
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Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850,
Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="genomic DNA"
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Mus musculus
                             genomic survey sequence.
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Matches 531; Conservative
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RRCI-24 Wouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BmH1 sites using MboI partially digested male C57BL/6J
DNA."
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library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC epage: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 330 row: A column: 6 Seg primer: SP6 Class: BAC ends.
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Larity 100.0%; Pred. No. 1.4e-148;
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/organism="Mus musculus"
                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-330A6"
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/strain="C57BL/6J"
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Best Local Similarity 99.4
Matches 308; Conservative
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BY091041 RIKEN full-length enriched, 10 days neonate heart Mus
musculus cDNA clone K630084E21 5', mRNA sequence.
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                                                                                                                                                                                                 CCAGACACTAAGICTGGAATGAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGCA 2184
CCAGACACTAAGTCTGGAATGAAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGCA 418
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 371)
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   479 GGCTGGTGTGGGGGGCTCCACAGGGCCAGTTCCAGGGGTTCATCACATGAGAAAA 537
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                                                                                                                                                                                                                                                                                                                                                        419 GGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATATAACG
                                                                                      TCACATITCTTCCTGATTCGCATACGCCGCGCCAGCTTGTCATCTCCCTCTTGGGCTTC
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URL:http://genome.gsc.riken.go.jp/
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Resploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY079997 RIKEN full-length enriched, 10 days neonate heart Mus musculus cDNA clone K630022E19 5', mRNA sequence.
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Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATATAACGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 racereceárcacreceárrecreacecererecreacecerececaaaceaareacerecea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2128 GACACTAAGTCTGGAATGAAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2188 GTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGGCTATATAACGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 TGGTGTGGAGGGCTCCACAGGGCCAGTTCCAGGGGTTCATCCACAAGAGAGAAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2008 TACGTGGGATGACTCGCATTGCTGAGCGGTGTGGTCACTGCCAAAGGAATGACCCTCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 306.8; DB 13; Length 371;
Pred. No. 1.8e-72;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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ORGANISM

REFERENCE AUTHORS

VERSION KEYWORDS SOURCE

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478 bp mRNA linear EST 19-JUL-2001
UI-R-DKO-cdj-f-07-0-UI.81 UI-R-DKO Rattus norvegicus cDNA clone
BI293043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2246 GCTGGTGTGGAGGGCTCCACAGGGCCAGTTCCAGGGGTTCATCCACAAGAGAGAAAAAC 2305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 GGGTGTGACTTGGCTTCCCAGGCTGGAAGAT--ATCTCACCAGCCCTACCTATATAACGG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 GCTGGTGTGGAGGGGCTCCACAGGCCAGTT-CAGGGGTTCATCCACAAGAGAGAAAAAC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 CAGACACTAAGTCTGGAATGAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGGCAG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: benco-soares@ulowa.edu

The sequence contained an oligo-dT track that was present in the oligonuclecide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the Noti site and the oligo-dT track served to identify it as a clone from the
                                                                                                                                                                                                      /dev_stage="10 days neonate"
/clone_lib="RIKEN full-length enriched, 10 days neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 478)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 CACATTICTICCIGATICGNATACGCCGCGGNCAGCTIGICATCTCCCTTTGGGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2126 CAGACACTAAGTCTGGAATGAAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2186 GGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATATAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2066 CACATTTCTTCCTGATTCGCATACGCCGCGGCCCAGCTTGTCATCTCCCTCTTGGGCTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2006 GATACGTGGGATGACTCGCATTGCTGAGCGGTGTGGTCACTGCCAAAGGAATGACCCTCT
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375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 9250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                DB 13; Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                         Score 269.6; DB 13;
Pred. No. 2.8e-62;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                         79 t
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Genome Res. 6 (9), 791-806 (1996)
97044477
organism="Mus musculus"
                                                                                               /db_xref="taxon:10090"
/clone="K630022E19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway rat)
                                                                                                                                                                      tissue_type="heart"
                                                                                                                                                                                                                                                                                                         102 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI293043.1 GI:14954159
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 95.5%;
Matches 298; Conservative
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SOURCE
ORGANISM
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DEFINITION
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ORIGIN
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VERSION
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TITLE
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Nikaido,T., Osato,N., Kasukawa,T., Adachi,J., Bono,H., Kodoo,S.,
Nikaido,T., Osato,N., Balto,R., Sutuki,H., Yamanaka,I., Kiyosawa,H.,
Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
Quackenbush,J., Schrimi,L.M., Kanapin,A., Marcauda,H., Batalov,S.,
Beisel,K.W., Blake,J.A., Bradt,D., Burusi,C., Chothia,C.,
Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,
A., Farzer,K.S., Gaasterland,T., Garibold,M., Jackson,I.J.,
Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M.,
King,B.L., Kongaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons
P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G.,
P.A., Maglott,D.R., Maltais,M., Porthouni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G.,
Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Tasadale
R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wanagisawa,M., Sakazuma,N., Wang,Y., Wangler,C., Wunshaw,Boris,A., Yanayi,Y., Yang,L., Yang,L., Yang,L., Waki,K., Kawai,J., Alzawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,
Y., Shinagawa,A., Yang,L., Yanguish,A., Yasaiki,D., Sasaki,D., Shibata,K., Shinayawa,A., Yasuishi,A., Yoshino,M., Waterston,R., Lander
R.S., Rogers,J. Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-resognsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Akimura, T., Arakawa,T., Komo,H., Miyazaki,A.,
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Saro,K., Shibata,K., Shiraki,T., Tagami,
M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
                                                                                                                                                                      Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare [ull-length cDNA libraries for rapid discovery of newgenes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepare mouse tissues. Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Yoshihide Hayashizaki
                                                                                                                                      Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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JOURNAL MEDLINE PUBMED COMMENT

TITLE

source

FEATURES

2125

61

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2185

121

2245

360

420

480

79

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Email: bento-soares@ulowa.edu

cDNA Library Preparation: M.B. Soares Lab Clone distribution:

clones will be available through Research Genetics (www.resgen.com)

This clone is also available through the I.M.A.G.E. Consortium at

LINL (inf@image.llnl.gov). IMAGE ID= 1790595 The following

repetitive elements were found in this cDNA sequence: 45-167,

>URRIA#DNA/MERI_type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                         254 CATCATGACTCATAACAGTAACACAATTACAGGCATGATGTAGCAATGAAATGATTTAT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 GGTTGAGGGTCACCACACATGAGGCCACCACACTGTTCTGGGGGAA---CAGTGGAGAG 138
   181 TICAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCCTCGACCCTTTGG 240
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/note="vector: pT7T3D-Pac (Pharmacia) with a modified
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
/note="vector: ptf-ref] not 1; Site_2: Eco RI; The UI-R-AGI
library is a normalized library constructed from 13 dpc
rat ventricle. The tag is a string of 6 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 434)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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UI-R-AG1-aal-b-08-0-UI.rl UI-R-AG1 Rattus norvegicus cDNA clone
UI-R-AG1-aal-b-08-0-UI 5', mRNA sequence.
                                                                                                                                                                                289 ------GTCACATATCATCTGTATATCAAAATATTCA
                                                                                                                                                                                                                                                         301 CATTACGATTCGTAACAGTAGCAAATTACAGGTATGAAATAGCAATGAAATAATTTAT
                                                                                                                                                                                                                                                                                                                                                                                        GATTGAAGGTCACCACAACATGAGGCCGCCACACTGTTCTAGAGAAAAATCACCTGGGTG
                                                                                                                                 241 GGGAATCAAACGACCCTTTACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 GGGAAAGGTTTGGGAAAGCCTTTCTGTCCATTCTTCATTCTTCAAAGTGATGTTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 AGGAAAGGATTGAGGAAGCC-TTCCATCTGTTCTGCACTCTTCAAAGGGATGTATTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 GAAAGCCTTTCAGCTGTTCTGCTGGGGCTCTTAGTAAGTCTGAGTAGGAACTGTA 535
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375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
71el: 319 335 8250
Fax: 319 335 9865
                                                                  332 Trcagggrcagccrgarrcragggcagcagrrcrcaaccrgga----
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Coordinated Laboratory for Computational Genomics
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF543101.1 GI:11634214
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TITLE
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/dev stage="AbULT"
/dev stage="AbULT"
/dev stage="AbULT"
/lab_host="bH10B (Life Technologies)"
ith a modified
polylinker; Site_I: Not I; Site_I: Bco RI; The UIR-DKO
library is a subfracted library derived from a mixture of
five individually tagged normalized rat libraries;
brain-nRBP (20%), haart-nRHP (20%), kidney-nRKP (20%),
acrea-nRAP (20%), and placenta-nRPP (20%). Each original
library was constructed from a mixture of equal amounts of
RNA from seven different developmental Lime-points:
embryonic day 1', adult day 12, adult day 75, and adult day
20 (Exception: the aorta pool does not contain embryonic
day 1' RNA and the placenta pool contains only the three
embryonic stages). Each library was normalized
individually according to the procedure described by
Bonaldo, Lennon & Soares (Genome Research Genome 6:
791-806, 1996). For construction of the five individually
tagged normalized libraries was mixed in the proportions
specified above and electroporated into competent bacteria
for production of single-stranded circular DNA
representing the pool of libraries. Single-stranded
circular DNA representing these five normalized libraries
was then used as a tracer in a subtractive hybridization
with a driver (PCR amplified inserts from a plasmid DNA
template preparation) comprising: a) a set of about 1,000
arrayed clones from each of the five normalized
libraries of brain (CTOs), heart (CSOs), kidney (CUO), aorta (CWOs), and placenta (CXOs). The resulting pool of about 2,000 arrayed
clones from each of the five normalized libraries of brain
(CTO), heart (CSO), kidney (CUO), aorta (CWOs), and
placenta (CXOs). The resulting pool of about 2,000 arrayed
TAG_LIBB-UI-R-DNO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GGTTCTGTCCCGAAGCTTCTCT 333
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normalized rat heart pool library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 170-292,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83;
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    .478
    organism="Rattus norvegicus"

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                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Seg primer: M13 Forward
POLYA=Yes:
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AW251306.1 GI:6594897
EST.
Rattus norvegicus (Norway rat)
                                                                                 >POLY A#Simple repeat
Seg primer: M13 Forward
POLYA=Yes.
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Best Local Similarity 78.4%;
Matches 261; Conservative
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AW251306/c
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UI-R-BJO-adx-e-05-0-UI.S1 UI-R-BJO Rattus norvegicus CDNA clone
UI-R-BJO-adx-e-05-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                  GCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATGATGATCACCACAACA 380
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: bento-soares@ulowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996. Tissue provided by Jim Lin, Department of Biology,
                                                                                                                                                                                                                                                                              CTGGAGTCACATATCATCTATCCTGTATATCAAATATTCACATCATGACTCATAACAGTA
                                                                                                                                                                                                                                                                                                                                                                           103 ACACAATTACAGGCATGATGTAGCAATGAATGATTTTATGGTTGAGGGTCACCACA
                                                                                                                                                                                                                                                                                                                                                                                                                     163 TGAGGCCACCACACTGTTCTGGGGGAA---CAGTGGAGAGGAAGGATTGAGGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    501 GCTGGGGCTCTTAGTAAGTCTGAGTAGGAACTGTATGTACCAGGTCTGCTTCTTATGGGT
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                                                                                                                                                                   Length 434;
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University of Iowa
175 Newton Road , 4156 MEBRF, Iowa City, IA 52242,
1781: 319 335 8250
Fax: 319 335 9565
                                                                                                         1 others
                                                                                                                                                                   Score 183; DB 10;
Pred. No. 1.6e-38;
0; Mismatches 96;
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                                                                                   University of Iowa."
94 c 103 g
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                                                                                                                                                                                    Best Local Similarity '... Matches 276; Conservative
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AW252440/c
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
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/clone="UT-R-BU0-add to the rechnologies" |
/clone="UT-R-BU0-add to the rechnologies" |
/lab_host="UH-R-BU0" |
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/clone lib="UT-R-BU0" |
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site="1: Not 1; Site=2: Eco R1; The UI-R-BU0 library is a subtracted library derived from the UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-BU0, at 16 dpc, ventricle at 16 dpc, AV canal at 16 dpc, and ventricle at 13 dpc, AV canal at 15 dpc, and ventricle at 13 dpc, AV canal at 16 dpc, and ventricle at 13 dpc, AV canal at 16 dpc, looked list and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996.

TAG_LIB=UI-R-BU0

TAG_LIB=UI-R-BU0

TAG_SEQ=GAAGG"

15 a ll cthers
      Library Preparation:
will be available
The following repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 17-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW251306
UI-R-BJO-adg-f-04-0-UI.sl UI-R-BJO Rattus norvegicus cDNA clone
UI-R-BJO-adg-f-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 ATGGAAACCAGAAGCCCAACAGTTGTCCTTCGATAGTGTCTCAGGACAGGCCAGGACAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 ----CACTAGGAGAGAGAGAACCCACGAAGGA-----TATCAGTGTGCTGGTTTTCCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 AATGTCTCATTCCGAAGGTTCTAGAAACACAGTTTACTGGATGAAGAGCTGAAGTGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  879 ATGAAAACGAGAAGACCAACAGTTATCCATTGATAGCGTCTCAGGACAGATAGGACAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     999 AATGTCTTGTACTGAAGATTCTAGAAACACAATTTGCTGGTTGAACAGCTGAAGTGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 GCCAGCAT----ACAAACATAACACCCTAATTAATGCTTCCCTCTGCTACTGACACCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                939 AGAACACTAGGAGAGGGGAACCCACGAAGGACAAGGTATTAGTGTTTGGTTTTCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55; Indels
normalized AV canal at 15 dpc library cDNA Librar M.B. Soares Lab Clone distribution: clones will through Research Genetics (www.resgen.com) The felements were found in this cDNA sequence: 1-44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; DB 9;
3.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1176 CTTCACTCTCTCTTTCATAAAAATAAAAAA 1208
                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cccrcacrcrrcrrrcaraaaraaacaass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 171;
Pred. No. 3
                                                                                                                                                                                                                                          Location/Qualifiers
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//note="Vector: prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | present | prints | present | prevent | prints | present | prevent | prints | present | prevent | prints | present | prints | present | prints | prevent | prints | prevent | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | prints | pri
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The sequence contained an oligo-dT track that was present in the oligonuclectide that was used to prime the synthesis of first strand CDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the CDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized ventricle at 13 dpc library CDNA bibrary Preparation:

M.B. Soares Lab Clone distribution: clones will be available elements were found in this CDNA sequence: 1-43,
                                                                                                                                 EST 04-JUN-1999
100 GCCAGCAT-----ACAAACATAACACCCTAATTAATGCTTCCCTCTGCTACTGACACACTT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 370)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI710529
UI-R-AG1-aal-b-08-0-UI.sl UI-R-AG1 Rattus norvegicus cDNA clone
UI-R-AG1-aal-b-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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/lab_host="DH10B (Life Technologies)"
/clone_lib="U1-R-AG1"
                                                                                                                                                                                                                                                                                                      1176 CTTCACTCTCTTTCATAAAAAAAAAAA 1208
                                                                                                                                                                                                                                                                                                                                                  CCTTCACTCTTCTTCATAAAATAAACAAACA 13

    .370
    /organism="Rattus norvegicus"

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97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Seg primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI710529.1 GI:5000305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Soares, MB
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
AI710529/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
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TITLE
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COMMENT
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//dev stage="dailt" |
//dev stage="dailt" |
//deb_host="DH10B (life Technologies)" |
//done=lib="UI-R-B10" |
//done=lib="UI-R-B10" |
//done=lib="UI-R-B10" |
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//note="Vector: pT71D-Pac (Pharmacia) with a modified |
//note="Vector: pT71D-Pac (Pharmacia) with a UI-R-B10 |
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//done=lib="Vector: pT-AB1, UI-R-AB1,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATGTCTTGTACTGAAGATTCTAGAAACACACAATTTGCTGGTTGAACAGCTGAAGTGGGGGT 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      879 ATGAAAACGAGAAGACCAACAGTTATCCATTGATAGCGTCTCAGGACAGATAGGACAGAG 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 ATGGAAACCAGAAGGCCAACAGTTGTCCTTCGATAGTGTCTCAGGACAGCCAGGACAGAG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   939 AGAACACTAGGAGAGGGGAACCCACGAAGGACAAGGTATTAGTGTGTTGGTTTTCAGGGC 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 ----CACTAGGAGAGAGAGAACCCACGAAGGA-----TATCAGTGTGTGTTTCCAGGGC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 AATGTCTCATTCCGAAGGTTCTAGAAACACAGTTTACTGGATGAAGAGGTGAGGGT 161
                                        Chordata, Craniata, Vertebrata, Euteleostomi,
Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: bento-soares@ulowa.edu
The sequence contained an oligo-dT track that was present in the oligouncleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized ventricle at 13 dpc library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                     1 (bases 1 to 511)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Iowa 375 Newton Road 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.3%; Score 171; DB 9; Length 511; 78.4%; Pred. No. 3.3e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10116"
/clone="UI-R-BJO-adg-f-04-0-UI"
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TAG_SEQ=CAGCGA"
120 c 113 g 151 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
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                                                                                                                                                                                                                                                                                                                        Genome Res. 6 (9), 791-806 (1996) 97044477
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TAG LIBBUI-R-BJO
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                                                                                         Mammalia; Eutheria;
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        Rattus norvegicus
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Best Local Similarity 83.6%;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 735)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                         ----CACTAGGAGAGGAGAACCCACGAAGGA-----TATCAGTGTGTGTTCCAAGGGC
                                                                                                                                                                                                                                                       117 GCCAGCAT----ACAAACATAACACCCTAATTAATGCTTCCCTCTGCTACTGACACTCT
                                                                                                           879 ATGAAAACGAGAGACCAACAGTTATCCATTGATAGCGTCTCAGGACAGATAGGACAGAG
                                                                                                                                                                      939 AGAACACTAGGAGGGGAACCCACGAAGGACAAGGTATTAGTGTGTTTGGTTTTCAGGGC
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                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU139209 AUACE1 Homo sapiens CDNA clone PLACE1010155 5', mRNA
                                            Score 167.8; DB 9; Length 370;
Pred. No. 2.2e-34;
0; Mismatches 57; Indeis 17;
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Genomics Laboratory
Hellix Research Institute
123-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
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mol_type="mkna"

db_xref="taxon:9606"

/clone="PLACE101015s"

/clone Tib="PLACE1"

/clone Tib="PLACE1"

/note="Vector: pME18SFL3"
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181 g 156
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                                              7.18;
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                                                                            Conservative
 82
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Matches 259;
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BASE COUNT
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/tssue_type="Thymus"
/dav_stage="4 weeks"
/dav_stage="4 weeks"
/dav_bost="Mulos"
/dlone_lib="Soares thymus_2NbMT"
/clone_lib="Soares thymus_2NbMT"
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IMAGE:3375590 5' Similar to gb:L35933 Mouse erythrocyte protein 4.2
(MOUSB);, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                       2165 ATTGGCCACTGGTGGGGGCAGGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCAC 2224
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 509)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1085194
                                                                                                                                                                                                                                                                            28 TCCCCTCCTTTCAGCTTCCCAGACACTGAGTCTGGAATGAAAATTCACCTGCCTCTGA
                                                                                                                                                                                                                        2105 TCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATTCACCTGCCTCTGA
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Pred. No. 4e-21;
               Length 735;
                                                                                                                      Indels
Score 131.8; DB 9;
Pred. No. 2.1e-24;
0; Mismatches 32;
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/clone="IMAGE:3375590"
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High quality sequence stop: 4
Location/Qualifiers
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/strain="C57BL/6J"
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/db_xref="GDB:7590285"
/db_xref="taxon:9606"
/clone="RPCI-11-236B22"
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Other GSSs: RPCI-11-236B22.TJ
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                                                                                                                                                                                                                                                                                                151; Conservative
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                                                                                                                                                          432 TACT-TTCACAGGGGTAGGCTATCAGGTATCCTGCATATCAGATATTTACATTATGATTC 374.
                                          192 CCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGGAATCAAAC 251
                                                                                                                                     311
                                                                                                                                                                                                                          312 GTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGTC 371
                                                                                                                                                                                                                                                      373 CTAACAGTAGCAAATTTATAGTTGTGAAGTAGCAATGAAATAAAGTTATGGTTGGGGGTC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. L (basea 1 to 538)
Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                    492 cccraccinadaccaccacircicaaccierececcicacciccirrececerrices
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      538 bp DNA 1111ca. ... semid UUGCIM library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse_10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                              252 GACCCTTTACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTACATTACGATTC
    Gaps
    1;
  39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2M0065I13R Mouse 10kb plasmid UUGC1M library Mu
clone UUGC2M0065I13 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bmail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0065 row: I column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
0; Mismatches
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Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 538.
Location/Qualifiers
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/clone="UUGC2M0065113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ804735.1 GI:12965546
                                                                                                                                                                                                                                                                                                                372 ACCACACATGAGG 385
                                                                                                                                                                                                                                                                                                                                                           313 Accacaacardage 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: plasmid ends
154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .538
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AZ804735/c
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LOCUS

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of pWD42 (gi|4732114 |gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptored vector DNA, and transformed into an elected to a majorially-competent B. coli Xii0-Gold (Stratagene) cells and selected for ampiciallin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 TTTACAGGGGTCACATATCATCTATCTATATGTCAGGTATTTACATTACGATTCGTAAC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 AGTACCAAAATTACAGTTTTGAAGTAGCAATGAATAATTTTTATGGTTGGAGGTCACCAC 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 522)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 ITCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGAATCAAACGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             390 Trchasdcaarcrcfcrcaaccracdgcrrfcaacccrrrggc----rarcaacccr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 TTCACAGGGGTCACATATCACATATTCTGCATGTCAGATATTTACATTACAGTTCATAAC
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Tel: 301 838 0200
Fax: 301 838 0208
Email: bb@ctigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
                                                                                                                                                                                                                                                                                                                                                                           4.9%; Score 116.2; DB 28; Length 538; 79.9%; Pred. No. 3.5e-20;
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Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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/organism="Homo sapiens"
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G 385
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AZ290439/c
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                                                                                                                                                                                                                                                                                                         1598 TTAGAACACGGTGAGCCTGTGGTGCACTAATTATGGCCAGTGACACCATAGAGTCAAAGT 1657
                                                                                                                                                                                                                                                                                                                                                                             1658 GCATTACTGAATGCTTTCAATTTCTCCTAATGCTGGTACGATGGCATGTCACAGGGCCAT 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Reesa ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Seq primer: SP6
                                                                                                                                                                                                                                                                    202 TCTATTTCTTGACCACTCTGATCCATTTTGAAGTAAAAATGCTCCAATTATTATGCTGTT 143
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 518)
                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                          82 GCATTACTGAATGCTTTCAATTTCTTATAATGATGGTGGCGTGGCATGTCATGGGCCTA 23
1540 TCTCTCTGTGCATCACTTCGGCCCGTTTTGGGGT--AGATCCTCTGATTAGCCTTCAGAT
                                                                                                                                                                                                                                                                                                                                             142 TTAGAACACGGTAAGCATGTCATGTGCTAATTATGGCCAGTGACATCATAAAAGAAAAGT
                                                                                                                                                                                               Gaps
                                                                                                                                                                                               7
                                                                                                                                                       Length 522;
                                                                                                                                                                                           45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Other GSSS: RPCI-23-449H23.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse BAC End Sequences from Library RPCI-23
Unpublished
                                                                                                                                                           Score 116; DB 28;
Pred. No. 3.9e-20;
                                                                                                                                                                                             0; Mismatches
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/organism="Mus musculus"
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/clone="RPCI-23-449H23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1718 TTTAGCTGCAGACATCACTCCA 1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 TTTAGCCCCAGACATCACTCCA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ114168.1 GI:7774139 GSS.
                                                                                                                                                           4.98;
76.78;
                                                                                                                                                                          Best Local Similarity 76.79
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: sro
Class: BAC ends.
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KEYWORDS
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AZ114168
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Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: szhao@tigr.org
Glones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
/note=Torgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
BCORI; Site 2: BCORI; Female C57BL/6J mouse kidney and/or
Brain genomic DNA was isolated and partially digested
with a combination of BCORI and BCORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
BCORI sites. The ligation products were transformed into
BHIOB electrocompetent cells (BRL Life Technologies).

94 c 108 g 158 t
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Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 CAGCAGTICTCAACCTGGGGGCCTCGACCCCTTTGGGGGAATCAAACGACCCTTTACAGG 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270 GGTCTCTTATCAAATATTCCACAAGTCAGATATGTATATTACAGTTTATAACAATGGCAA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325 AATTACAGGTATGAAATAGCAATGAAATAATTTTATGATGATGAGGTCACCACAACATGAG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 AATTCCAGTTATGAGGGAGTAATGAATAATTTTATAGTTGAGGGTCATCACAACATGAG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 596)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 CAGTGGTTCTCAACCTGTGGGTCGCGACCCCTGTGGGGGGATTTACTGTCCCTCTCCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 ACAAGGIGCICATIGGGAAITICCIGGAGCIICICITICAGGAICAGCCIGAIICIAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 ACAGGCCATGCATTTTGAAAGGCTTAGTGTTCTTGATTTTTAACACTACTTTGACGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                          h 4.9%; Score 114.6; DB 28; Length 518; Similarity 67.2%; Pred. No. 9.4e-20; 62; Conservative 0; Mismatches 79; Indels 0;
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Other GSSs: RPCI-23-59G22.TJB
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ290439.1 GI:9532225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seg primer: T7
Class: BAC ends.
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/use in the comparison of the products with a combination of Ecori selection of Ecori and or Ecor in the combination of Ecor in the partially digested with a combination of Ecor and partially digested with a combination of Ecor and Ecor in the partially digested with a combination of Ecor and Ecor in the partially digested with a combination of Ecor and Ecor in the partially digested with a combination of Ecor and Ecor in the partially digested with a combination of Ecor and Ecor in the partially digested with a combination of Ecor and Ecor in the partially digested but a cloned into products were transformed into DHIOB electrocompetent cells (BRL Life Technologies).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 4.8%; Score 113; DB 28; Length 596; Best Local Similarity 78.3%; Pred. No. 2.7e-19; Matches 148; Conservative 0; Mismatches 40; Indels 1
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        379 CATGAGGCC 387
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